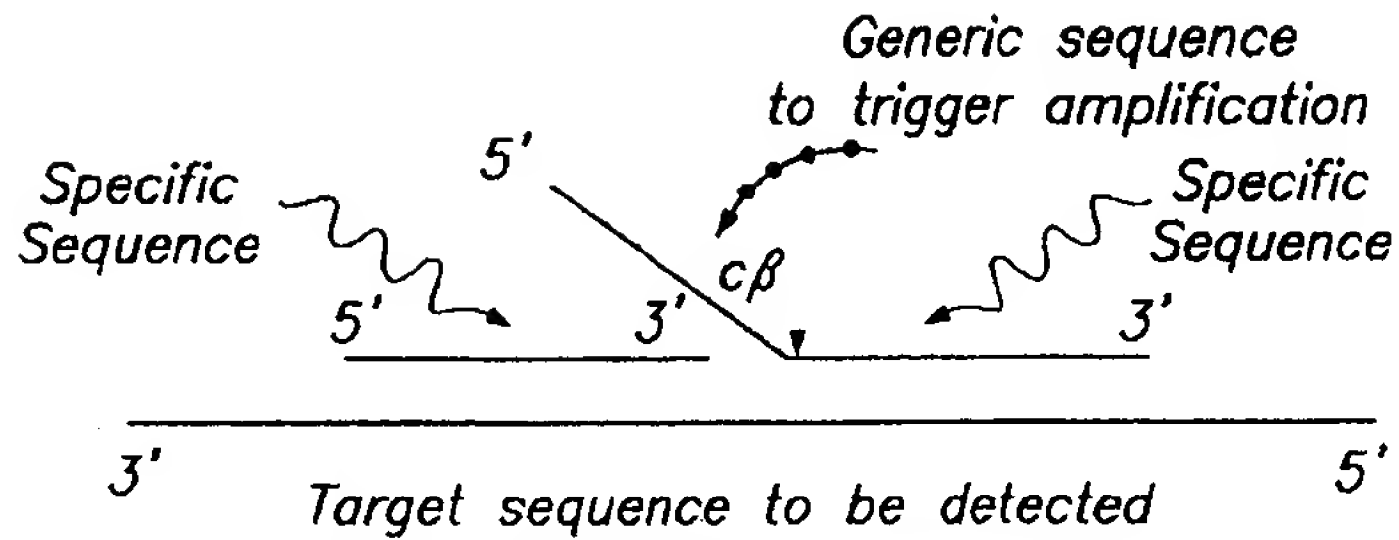
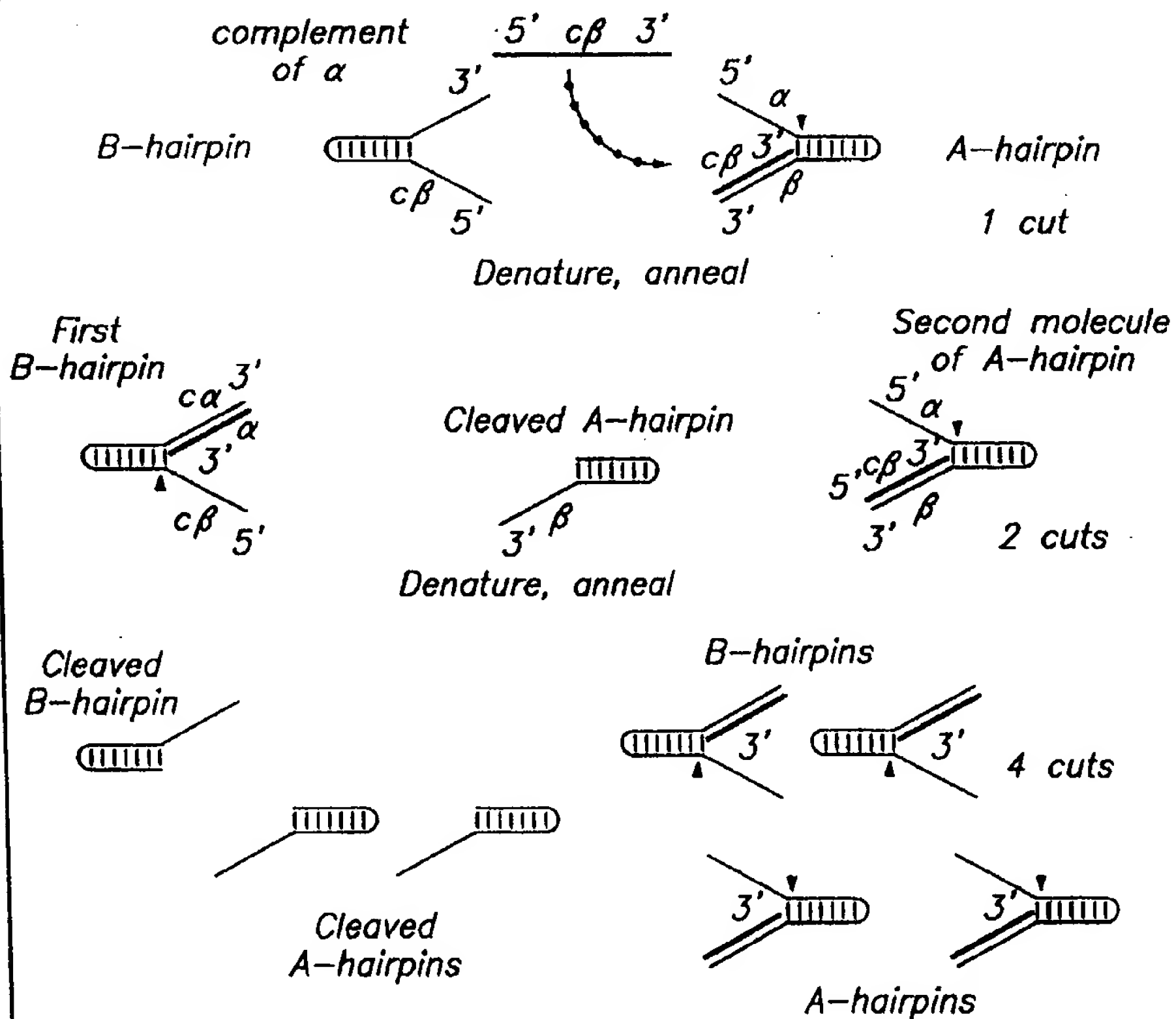


FIG. 1A



**FIG. 1B** PART ONE: TRIGGER REACTION



**FIG. 1C** PART TWO: DETECTION REACTION

090409Z . 022602

DNAPIAQ	[SEQ ID NO:1]	A G . G . . . . . G . . . . .	G . . . . .		70
DNAPTFL	[SEQ ID NO:2]	. . . . .	C . G . . . . .		67
DNAPTTH	[SEQ ID NO:3]	G A . . . . . G . . . . . A . . . . .			70

DNAPIAQ	CA	6	140
DNAPIFL	T	6	137
DNAPIIH		6	140

DNAPIAQ	.....	C	.....	A	207
DNAPIFL	.....	A	.....	GT	204
DNAPTTH	.....	I	AA	GT	210

DNAPTAQ	G.	GG.	G.	277
DNAPTFL	.	.	.	274
DNAPTTH	GA.	G.	G.	280

DNAPIAO	A.	.	.	.	.	.	.	G.	.	.	.	G.		347
DNAPIFI	G.	.	.	T.	.	.	.	A.	G.	.	T.	G.	.	344
DNAPITH	.	.	.	.	.	.	.	I.	A.	C.	.	.	.	350

FIG. 2B

MAJORITY [SEQ ID NO:7]	CGAGGCGGAGGAGGTGCTGGCCACCGTGGCCAAAGAAAGGCGGATACGAGGTGGGCATCCTC	
DNAPTAG [SEQ ID NO:1]	.....C.....G.....C.....C.....	417
DNAPTFL [SEQ ID NO:2]	T.....G.....CG.....	414
DNAPTTH [SEQ ID NO:3]	.....T..C.....	420
MAJORITY ACCGCGGACCGGAGGCTCTAGGAGTGGTTCCGACCGCATGGGCTCTCCACCCGAGGGGTACCTCA		
DNAPTAG	.....AAA.....T.....CA.....	487
DNAPTFL	..T.....A.....G.....G.....A.....T.....G.....	484
DNAPTTH	.....A.....G.C.....G.....CC.....	490
MAJORITY	TCACCCGCGGCTGGCTTGGGAGAAATACGGGCTGAGGCGGAGCAATGGGTGGACTACCGGGCCCTGGC	
DNAPTAG	.....C.....A.....A.....C.....C.....CG.....A.....	557
DNAPTFL	.....AC.....C.C.....	554
DNAPTTH	.....A.....C.....T.....C.....C..T	560
MAJORITY	GGGGAGCGGCTCGGACAACTCCCGGGGTCAAGGGCATGGGGAGAGAGCCGCCXGAAGCTCCTCXAG	
DNAPTAG	C.....GAG.....T.....G.....GAG.....T..GG..	627
DNAPTFL	.....G..T..A.....G.....A.....A..G....A..CGC	624
DNAPTTH	.....TC.....TC.....A..	630
MAJORITY	GAGTGGGGAGGCTGGAAACCTCCTCAAGAACTGGACCGGGTGAAGGCCCGC...CXTCGGGAGAGAGA	
DNAPTAG	.....GC.....C.....A.....	684
DNAPTFL	.....T..C..C.....A.....T..G.....C	691
DNAPTTH	.....A.....A.....A.AAAA.G.....	700

FIG. 2C

MAJORITY [SEQ ID NO:7] TCCAGGCCACATGGAXGACCTGAXGCTCTCTGGGAGCTXTGCCAGGTGGGACCGAGCCTGGCCCTGGGA

DNAPTAG [SEQ ID NO:1] ...T...C...T...A...C...GG...A... 764  
 DNAPTFL [SEQ ID NO:2] ...GG...G...C...GCC...T...C...A...T...A...T... 761  
 DNAPTTH [SEQ ID NO:3] ...A...C...A...C...G...T...C...G...C... 770

MAJORITY GGTGGACTTGGGCAAGXGGGGGAGGCGGACGCGGAGGGGCTTCTGGAGAGGCTGGAGCTT

DNAPTAG ...AA...AA...A...T...A...T...T...T...T... 834  
 DNAPTFL ...GG...G...C...C...CACA...A...T...T...GG...T...C...T... 831  
 DNAPTTH ...C...C...G...G...G...G...G...G...G...G...G...C... 840

MAJORITY GGGAGGCTGCTGCAGGAGTTCGGGCTCTCTGGAGGGGGCGGAGGCGGCTGGAGGAGGCGGCTGGCCCGCGG

DNAPTAG ...T...T...AA...T...AA...T...T...T...T... 904  
 DNAPTFL ...A...T...G...G...G...G...G...G...G...G...G...T... 901  
 DNAPTTH ...G...G...G...G...G...G...G...G...G...G...G... 910

MAJORITY CGGAAGGGGCTTGGTGGGCTTGTGCTTTCGGGGCGGAGGCGGCTTCTGGCCCTGGC

DNAPTAG ...T...T...G...G...AAG...T...T...T...T... 974  
 DNAPTFL ...T...T...T...T...T...T...T...T...T...T... 971  
 DNAPTTH ...G...G...G...G...G...G...G...G...G...G...AAA... 980

MAJORITY GGGGCGCAGGGGCGGGGTGGACCGGGGACGACGCGCTTAXGGGCTTAXGGGACCTXAGGAGGCTG

DNAPTAG ...G...G...G...G...G...G...G...G...G...G...G...C... 1044  
 DNAPTFL ...GG...GT...G...GG...T...A...G...G...G...G...T...G... 1041  
 DNAPTTH ...TG...C...G...G...G...G...G...G...G...G...G...G...C... 1050

[illegible]

FIG. 2E

MAJORITY [SEQ ID NO:7] GGAGATCCGCGCCCTCGAGGAGGTCCTTCGGCGTGGCGGGGCGGCGCTTCAAGCTCAAGTGGCGGGGAC

DNAPTAQ [SEQ ID NO:1] .....CC..... 1464  
 DNAPTFL [SEQ ID NO:2] .....AG..G..... 1461  
 DNAPTTH [SEQ ID NO:3] .....T...G..... 1470

MAJORITY CAGCTGGAAAGGCTGCTTTCAGGAGGCTXGGGCTTCGGCGCATCGGCAAGACGGAGAGACXGGCAAGC

DNAPTAQ .....C.....A.....C..... 1534  
 DNAPTFL .....GC.....G..C..G..T.....G..G..A.. 1531  
 DNAPTTH .....TA.....T..G..G.....C..A.....A..... 1540

MAJORITY BCTCCAGGAGCGCGCGCTGCTGGAGGCGCTXCGXGAGGCGCGCCCATCGTGGAGAGATCCTGCAGTA

DNAPTAQ .....C.....C..C..... 1604  
 DNAPTFL .....T.....G..A.....CGGC..... 1601  
 DNAPTTH .....G.....A..G.....C...C.. 1610

MAJORITY CGGGAGGTCAGCAAGCTCAAGAGACAGCTACATXGAGCGCGCTGCGXGCTGCTGAGCGCGAGCGGGC

DNAPTAQ .....B.....B.....T.....G..A.....A..... 1674  
 DNAPTFL .....A.....A.....C..C..G.....A...C... 1671  
 DNAPTTH .....G.....G..G.....C..AAG.....G..... 1680

MAJORITY CGCCTCCACACCGCGCTTCAAGCAGACGGCCACGGCGCAGGCTTAGTACCTCGAGCGCCCAACCTGC

DNAPTAQ .....A.....A.....T.....C.. 1744  
 DNAPTFL .....G.....C.....TCC..... 1741  
 DNAPTTH .....G.....G..... 1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAAATCCCGTCCGACCCXCTGGGCGAGGATCCGGGGGCTTGGTGGCCBAGGAGGGXTGGGT	
DNAPIAQ [SEQ ID NO:1]	.....G..T..G.....A..C.....G...C.	1814
DNAPTFL [SEQ ID NO:2]	.....G.....T.....C..C.....A.....C.....	1811
DNAPTTH [SEQ ID NO:3]	.....CT.....C.....C.....T.....C.....	1820
MAJORITY	GTGGTGGCCCTGGACTATAGCCAGATAGAGCTCGGGGTCTGGCCGAGCTCTCCGGGAGGAGAGCTG	
DNAPIAQ	A.....A.....A.....G.....C.....	1884
DNAPTFL	.....T..T.....C.....T.....T.....	1881
DNAPTTH	.....C.....C.....C.....A.....	1890
MAJORITY	ATCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACGGGAGCTGGATGTTGGGCTCCGCCCGG	
DNAPIAQ	.....C.....G.....GG.....G...	1954
DNAPTFL	.....T.....T.....T.....T.....C.	1951
DNAPTTH	.....A.....A.....A.....	1960
MAJORITY	AGGGCTGGACCCCTGATGGCCGGGGCCGAGACCATCAACTTCGGGCTCCTCTAGGGCATGTCCGG	
DNAPIAQ	.....A..G..A.....T.....G...	2024
DNAPTFL	.....A.....T.....GG..G.....G.....	2021
DNAPTTH	.....G.....G.....G.....G.....	2030
MAJORITY	CCACGGCTCTCCAGGAGCTTGGCATCCGCTACGAGGAGGGGTGGCCCTTCATTGAGGCTACTTCCAG	
DNAPIAQ	.....A.....T.....CCA.....T...	2094
DNAPTFL	.....GG.....T.....	2091
DNAPTTH	...TA..G.....T..A.....A.....A	2100



# FIG. 2G

MAJORITY [SEQ ID NO:7] AGCTTCCGCAAGGTGGGGGCTGGATTGAGAAAGCCCTGGAGGAGGCGGCGGTACGTTGGAGA

DNAPTAQ [SEQ ID NO:1] ..... 2164  
 DNAPTFL [SEQ ID NO:2] ..... 2161  
 DNAPTTH [SEQ ID NO:3] ..... 2170

MAJORITY CCGTCCTTGGGGCGGGGGCTACGTGCGCGAGCCTCAAGGCGCGGGTGAAGAGCGGTGGGGGAGCGCGGGGGA

DNAPTAQ ..... 2234  
 DNAPTFL ..... 2231  
 DNAPTTH ..... 2240

MAJORITY GCGCATGGCCCTTCAACATGCCCGTCCAGGGCCACCGCGCGACCTCATGAAGCTGGCGCATGGTGAAGCTC

DNAPTAQ ..... 2304  
 DNAPTFL ..... 2301  
 DNAPTTH ..... 2310

MAJORITY TTCCCGCGGCTXCAGGAAATGGGGGCGAGGATGGTGGTCAAGGTCCAGGAGGAGCTGGTGGTGGAGGGCC

DNAPTAQ ..... 2374  
 DNAPTFL ..... 2371  
 DNAPTTH ..... 2380

MAJORITY CCAGAGCGGGCGGAGCGGTGGCGGCTTGGCCAGGAGGTGATGGAGGGGCTATCCCGCTGGCGGT

DNAPTAQ ..... 2444  
 DNAPTFL ..... 2441  
 DNAPTTH ..... 2450

# FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGACGCTGGACGCTGGGGATGGGGGAAGACTGGCTCTCGGGCCAAAGGAGTAG	
DNAPTAD [SEQ ID NO:1]	.....A.....	GA 2499
DNAPTFL [SEQ ID NO:2]	.....CC.....	2496
DNAPTTH [SEQ ID NO:3]	.....T.....	GT... 2505

FIG. 3A

MAJORITY [SEQ ID NO:83]		MXAMLP	IFEPKORVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLLKALKEDG	DAVXVVFDAK
TAQ PRO	[SEQ ID NO:4]	RG	H	69
TFL PRO	[SEQ ID NO:5]		V	68
TTM PRO	[SEQ ID NO:6]	E	YK	70
MAJORITY APSFRHEAYEAYKAGRAPTPEDFPROLALIKELVDLGLXRLEVPQYEADDOVLATLAKKAEKEGYEURIL				
TAQ PRO		GG	A	139
TFL PRO		V	F	138
TTM PRO		FT		140
MAJORITY TADRDLYQLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKSIGENTAXKLLX				
TAQ PRO		K	H	209
TFL PRO		E	I	208
TTM PRO		V	V	210
MAJORITY EWGSLNLLKNLBRVXPXXREKIXAHMEDLXLSXXLSXVRTOLPLEVDFAXRREPDRGLRAFLELEF				
TAQ PRO		A	L	278
TFL PRO		FQH	Q	277
TTM PRO		ENV	K	280
MAJORITY GSLIHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEILLALAAARXGRVHRAXDPLXGLRDLKEV				
TAQ PRO		S	S	348
TFL PRO		B	A	347
TTM PRO		A	AP	350

FIG. 3B

MAJORITY [SEQ ID NO:8] RGLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGWTEGAGERALLSERLFXNLXX

TAQ PRO	[SEQ ID NO:4]	S.....G.P.....	.....F.....	.....A.....	.....A.....	WG	418
TFL PRO	[SEQ ID NO:5]	I.....F.E.....	.....A.....	.....A.....	.....QT.....	KE	417
TTN PRO	[SEQ ID NO:6]	.....S.....V.....	.....AH.....	.....HR.....	.....LK	420	

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD

TAQ PRO	R.....R.....A.....	.....R.....	.....A.....	.....	488
TFL PRO	K.....E.....R.....	.....EA.V.Q.....	.....	487	
TTN PRO	.....K.....H.....	.....L.....	.....	490	

MAJORITY QLERVLFDELGLPAIGKTEKTKRSTSAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG

TAQ PRO	.....S.....D.I.....	558
TFL PRO	.....DR.....A.....K.....	557
TTN PRO	.....R.....L.....Q.....H.....V.....S.....	560

MAJORITY RLHTRFNOTATATGRLSSSDPNLONI PVRTPLGQRI RRAFWAEEGWXLVALDYSOIELRVLAHLSGDENL

TAQ PRO	.....L.....	628
TFL PRO	.....V.....V.....	627
TTN PRO	.....A.....A.....	630

MAJORITY IRVFQEGROIHTQTASWMFGVPEAVOPLMRAAKTINFGVLYGMSAHLSDLAIPYEEAVAFIERYFD

TAQ PRO	.....E.....R.....	698
TFL PRO	.....S.....G.....S.....	697
TTN PRO	.....K.....V.....	700

FIG. 3C

MAJORITY [SEQ ID NO: 8] SFPKVRAWIEKTLSEGRBGGYVETLFGRRRYVPDLNARVKSUREAERMAFNMPVQGTADLKKLAMVKL

TAQ PRO	[SEQ ID NO: 4]	.....E.....	768
TFL PRO	[SEQ ID NO: 5]	Y.....6.....R.	767
TTH PRO	[SEQ ID NO: 6]	.....K.....	770

MAJORITY FPRXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAQ PRO	.....E.....E...A...R.....I.....	833
TFL PRO	.....Q.L.....D...R.....W...Q.....L.....	831
TTH PRO	.....R.....L.....QA...E...A...KA.....M.....G	835

Genes for Wild-Type and Pol(-)DNAPTaq

Domain  
Coding Regions: 5' Nuclease

Polymerase

FIG. 4A

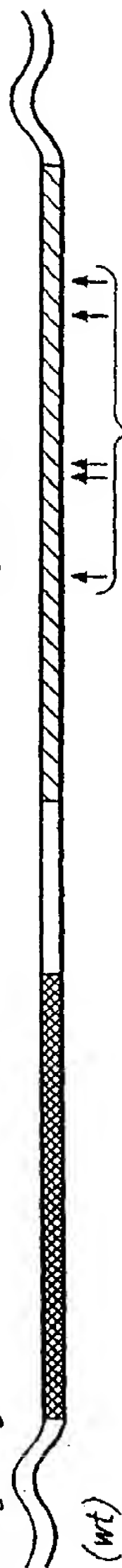


FIG. 4B

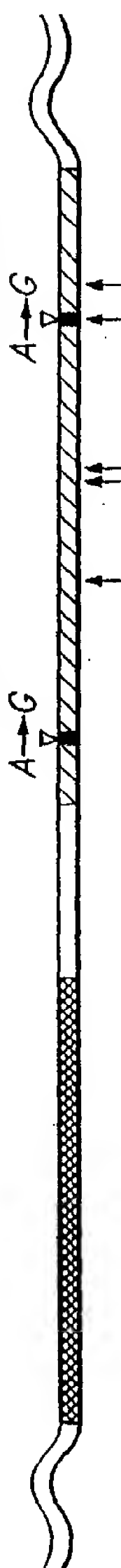


FIG. 4C



FIG. 4D

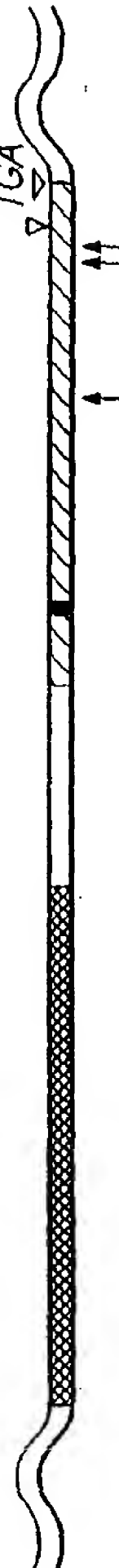


FIG. 4E



FIG. 4F

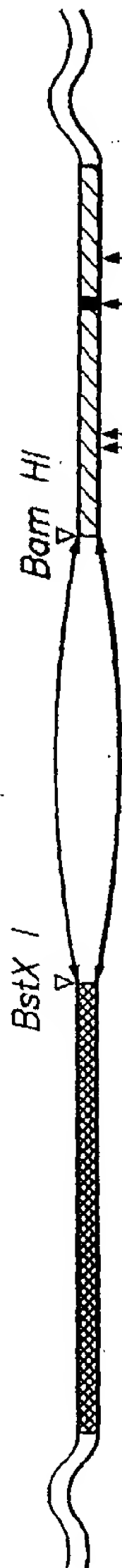
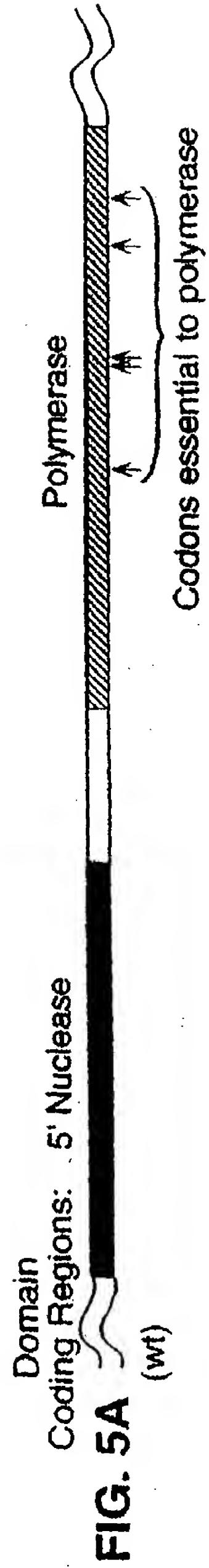


FIG. 4G



# Genes for Wild-Type and Pol(-) DNAPTfl



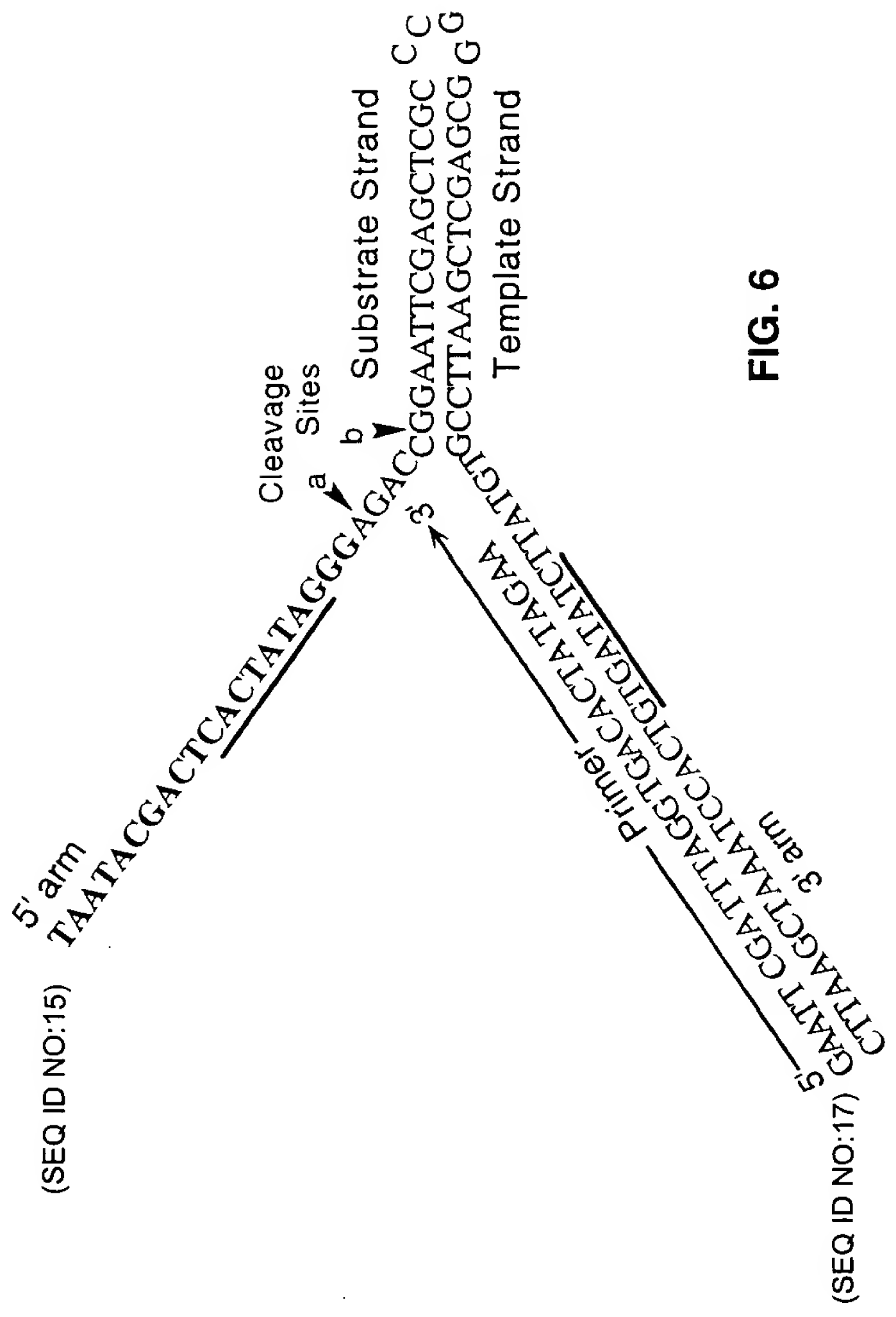


FIG. 6



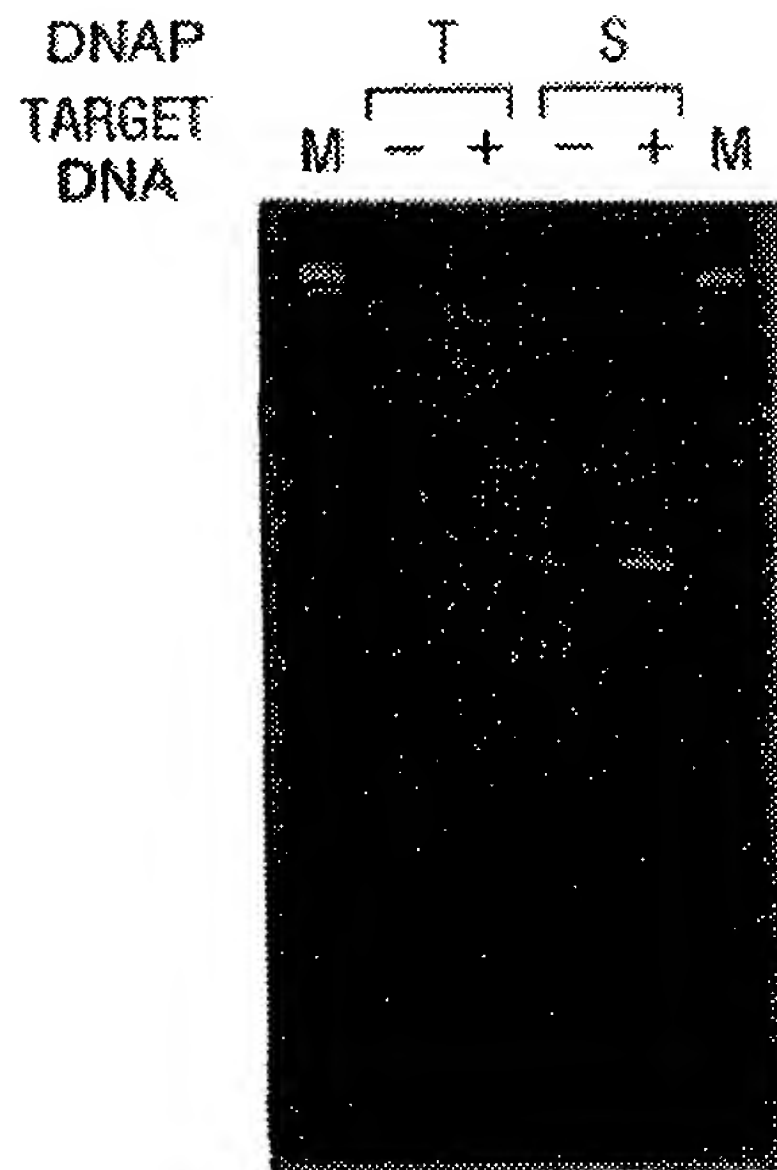


FIG. 7

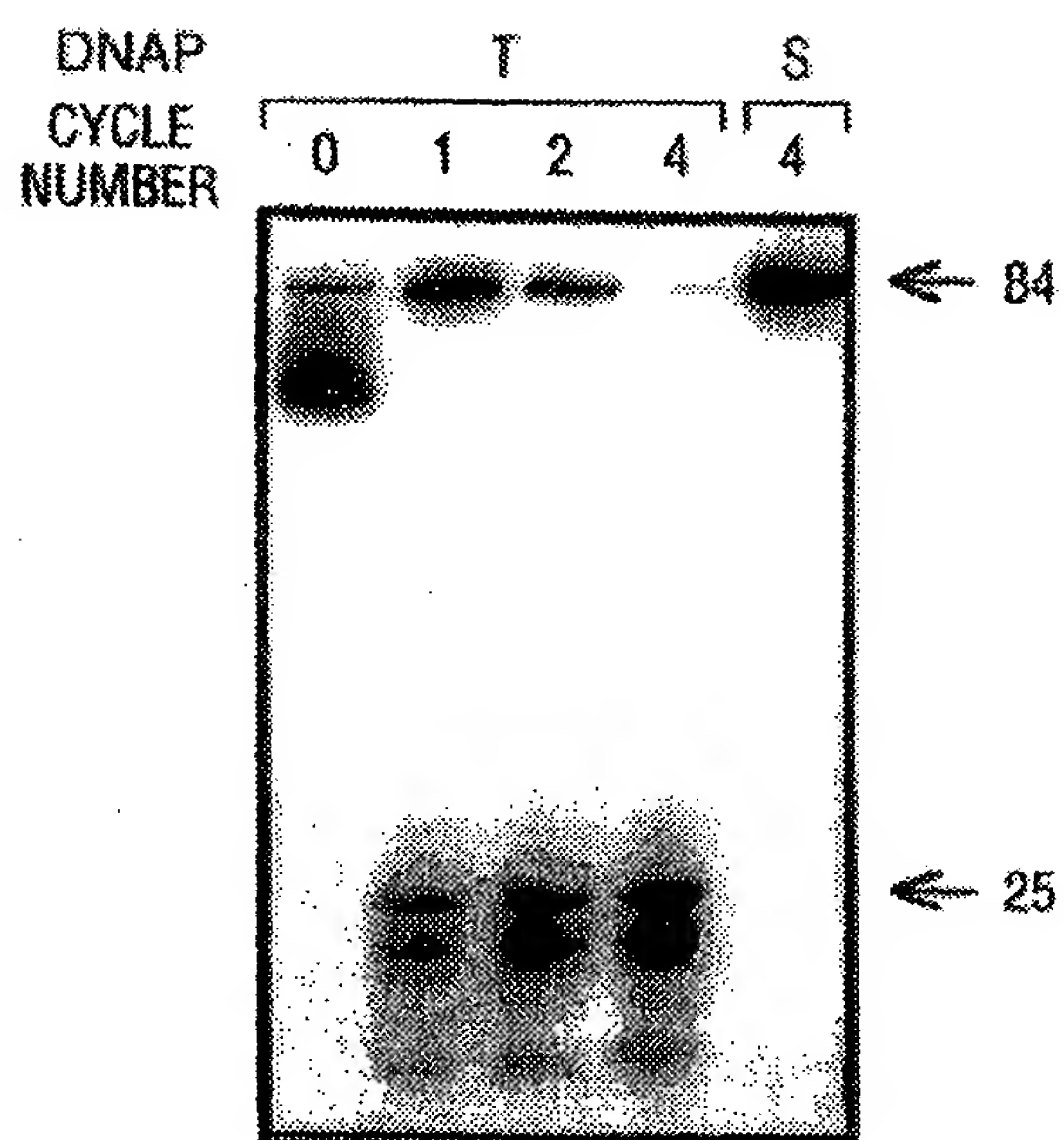


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

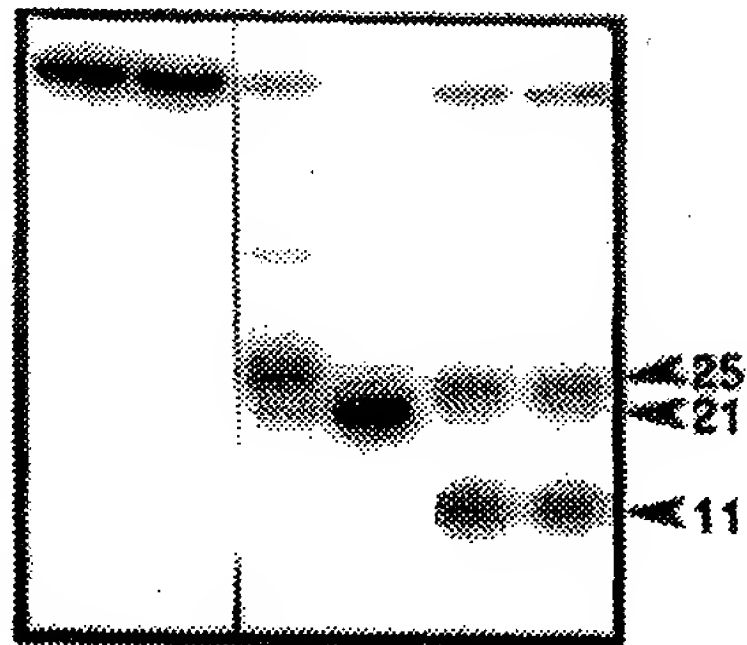


FIG. 9A

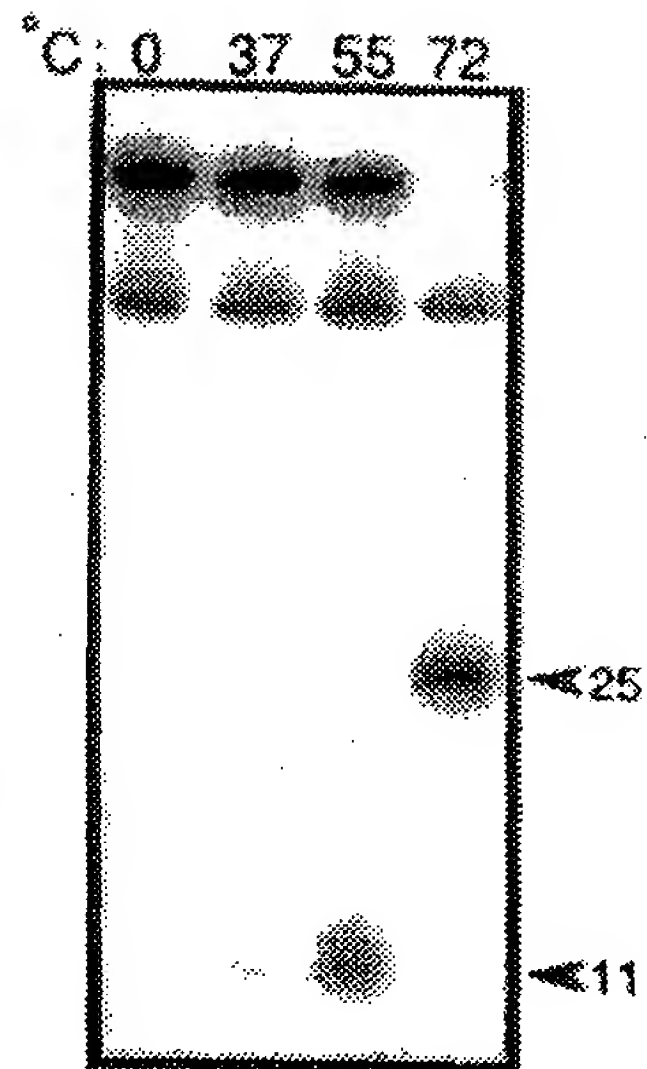


FIG. 9B

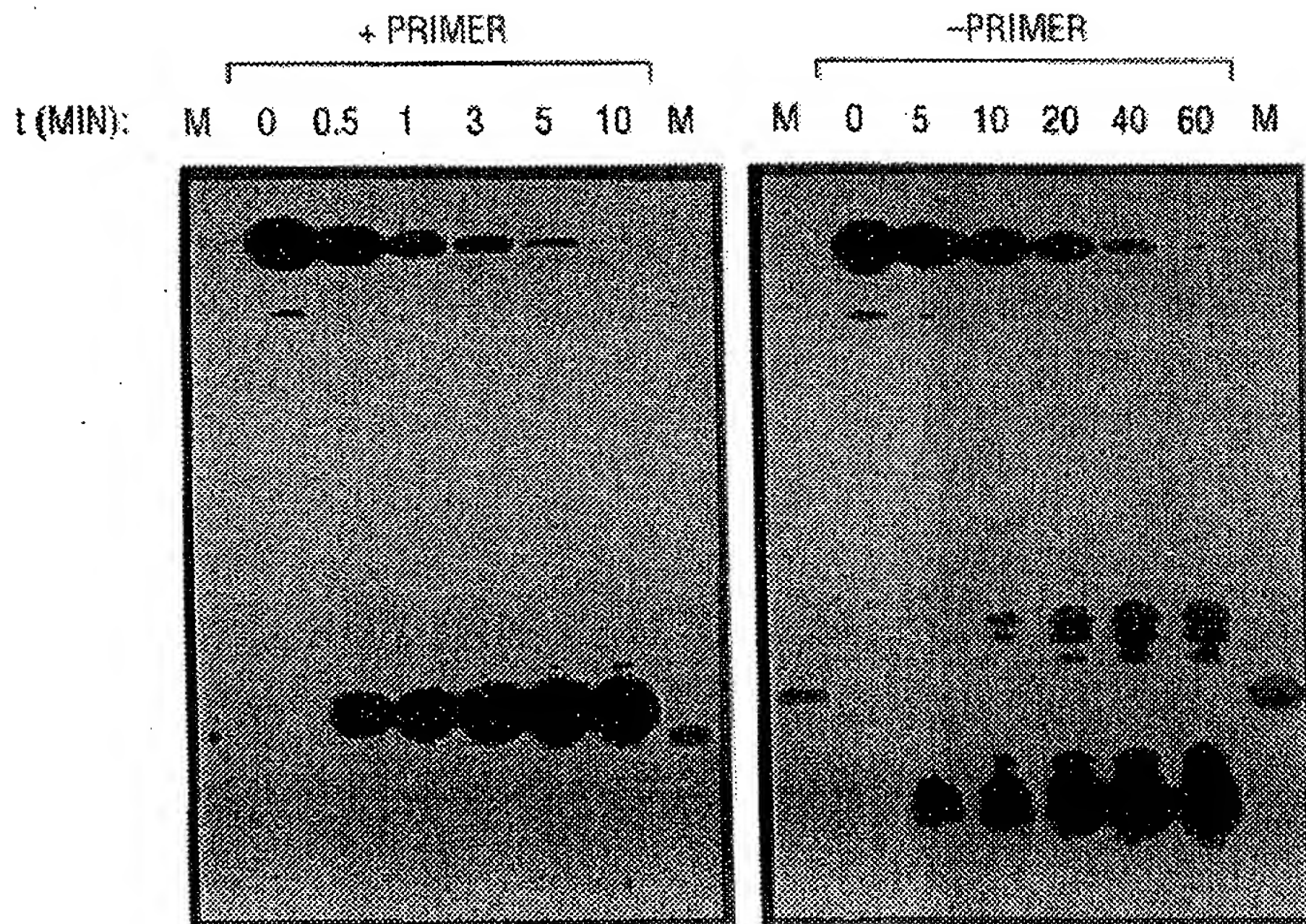


FIG. 10A

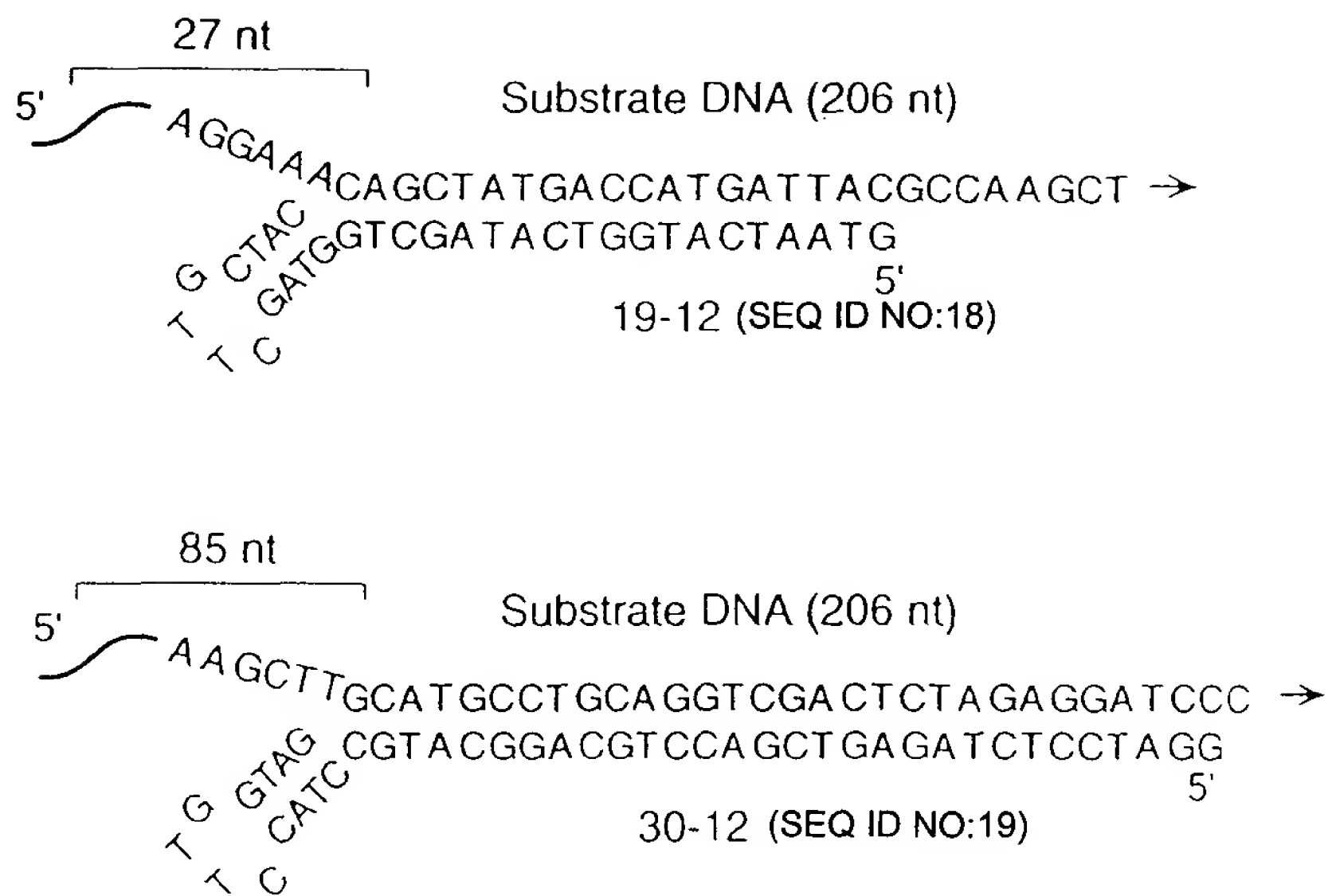
FIG. 10B



FIG. 11A

FIG. 11B

FIG. 12A



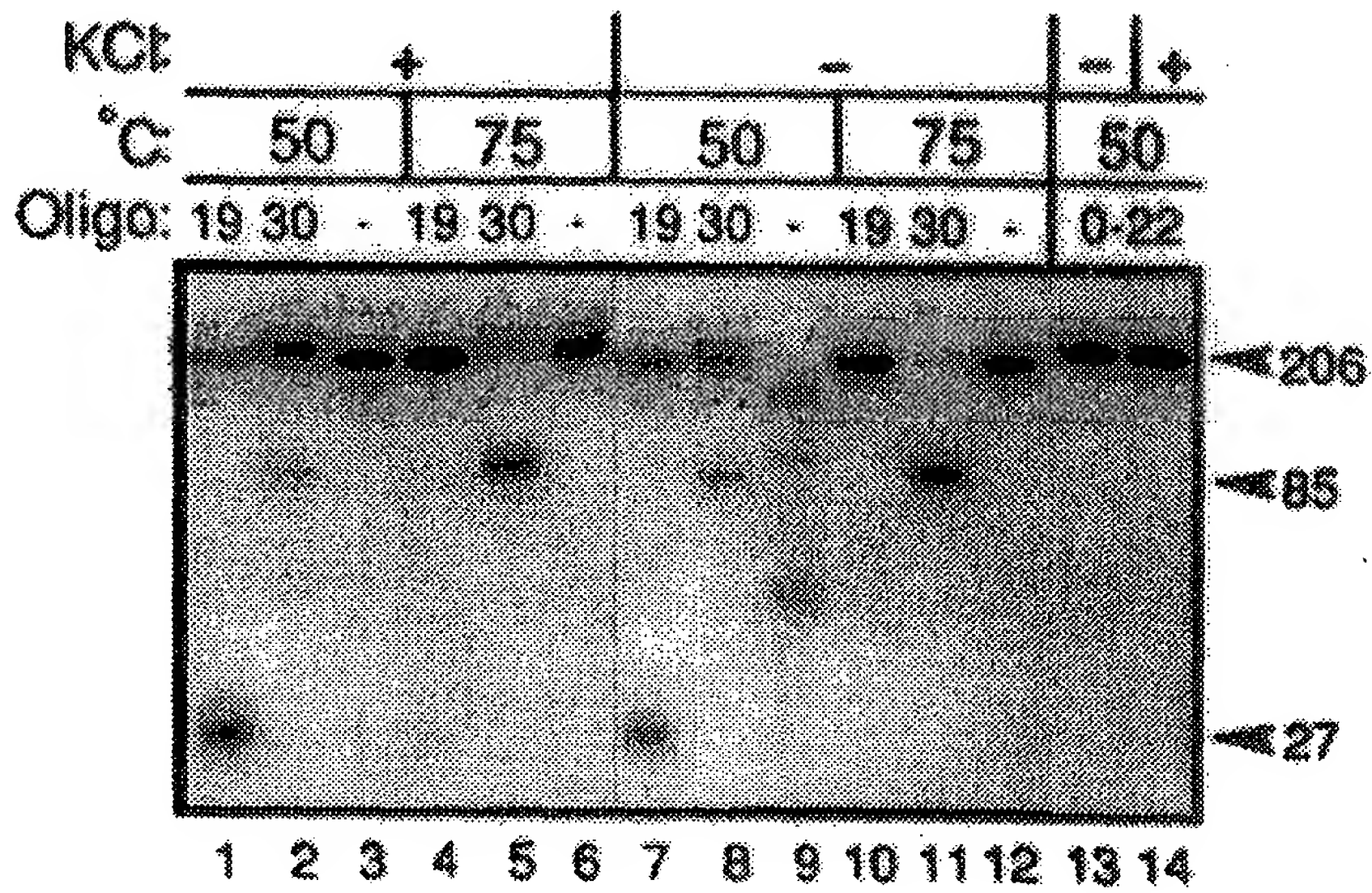


FIG. 12B

DNAP: -   +   +  
 30-0 : -   -   +

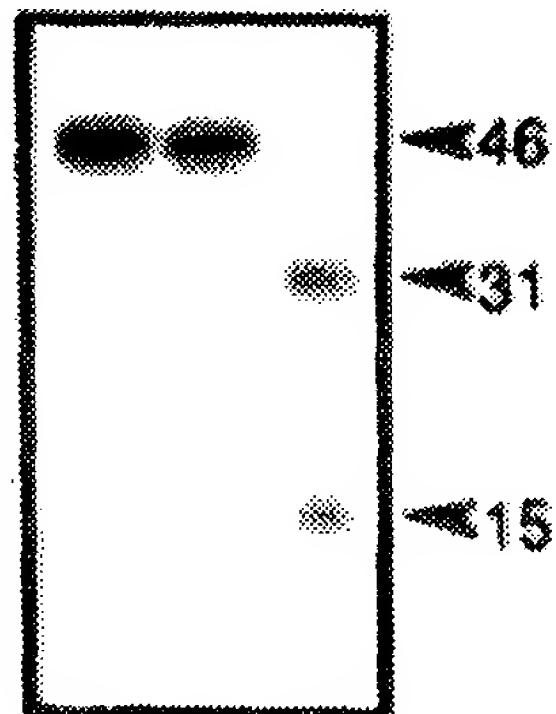
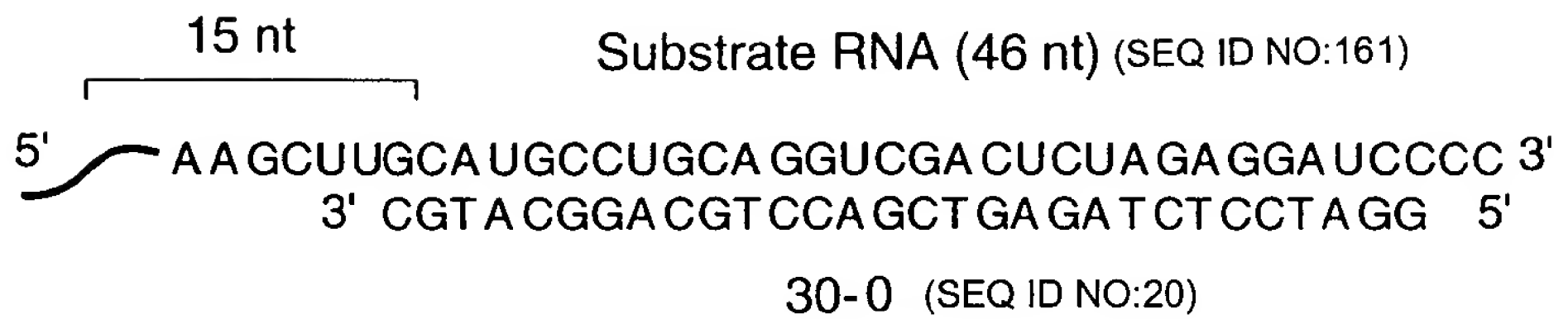


FIG. 13B

**FIG. 13A**



(SEQ ID NO:162)

-35  
-10  
RBS

TTGACAAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAAATTTACACACAGGAACAGCG

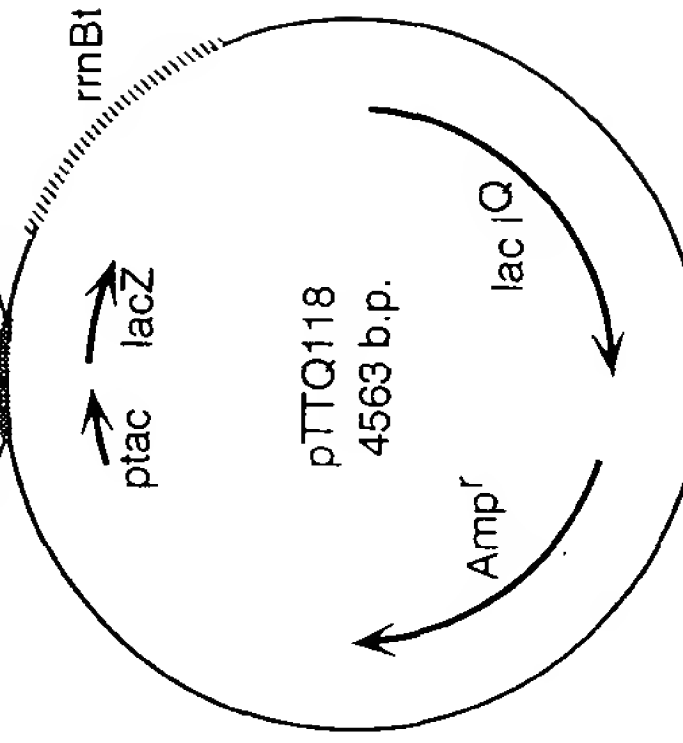
MetAsnSer...

ATGAATTTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCC

EcoRI KpnI BamHI SalI SphI HindIII

SstI SmaI XbaI PstI

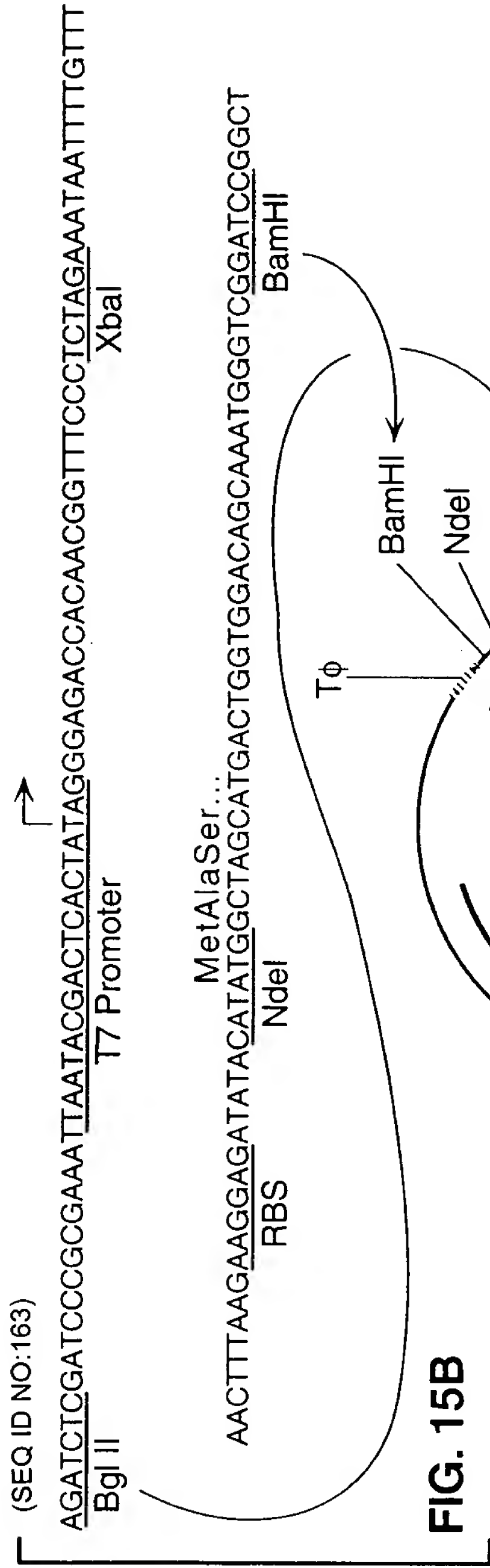
FIG. 14B



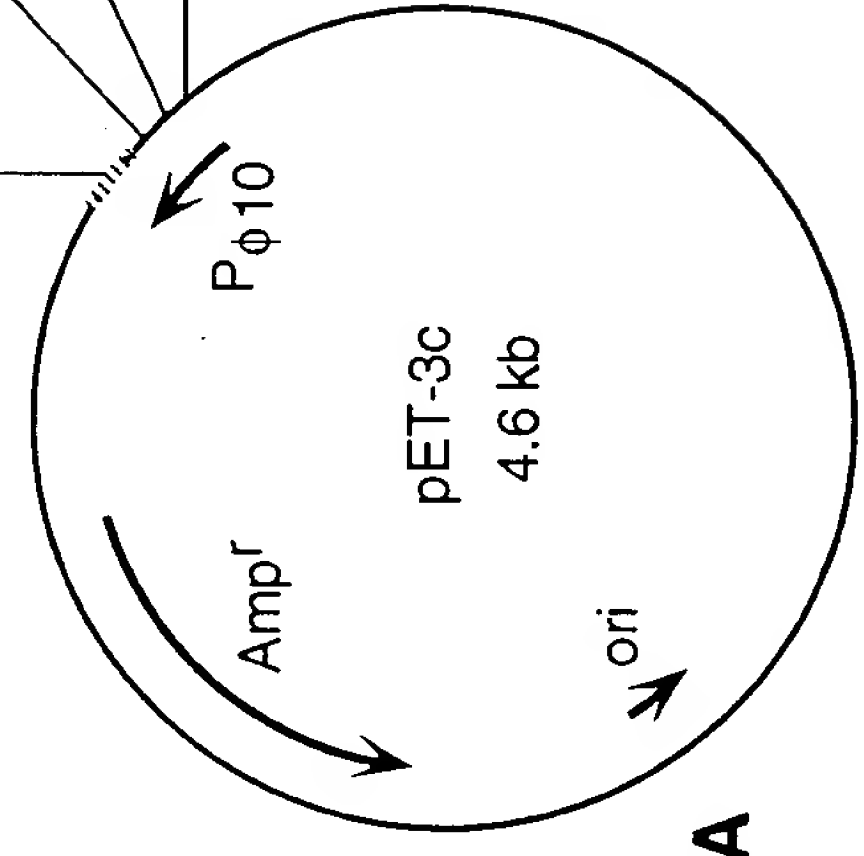
**FIG. 14A**

RBS: Ribosome binding site  
ptac: Synthetic tac promoter  
lac I<sup>Q</sup>: Lac repressor gene  
lacZ: Beta-galactosidase alpha fragment  
rrnBt: E. coli rrnB transcription terminator

**FIG. 14C**



**FIG. 15B**



**FIG. 15A**



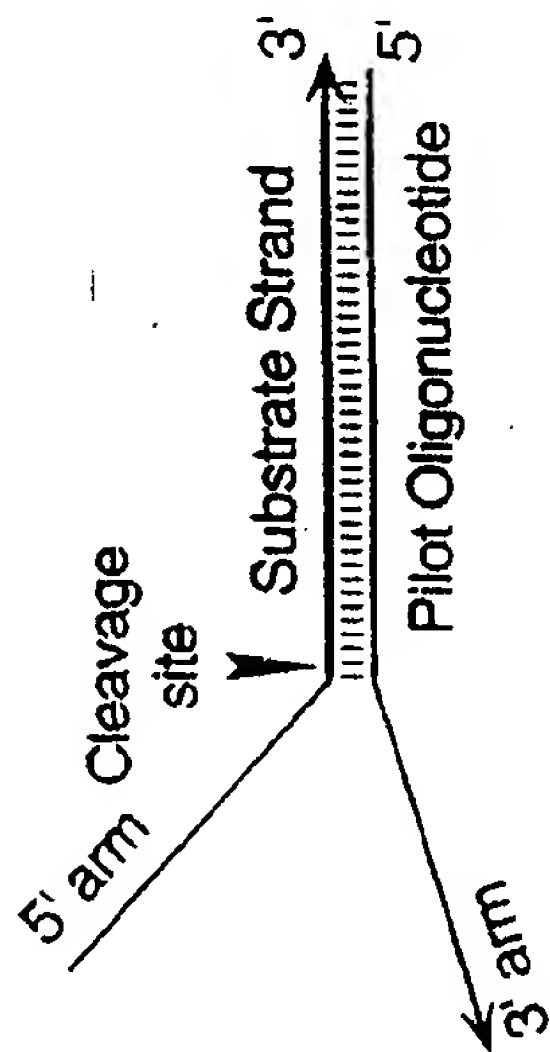


FIG. 16A

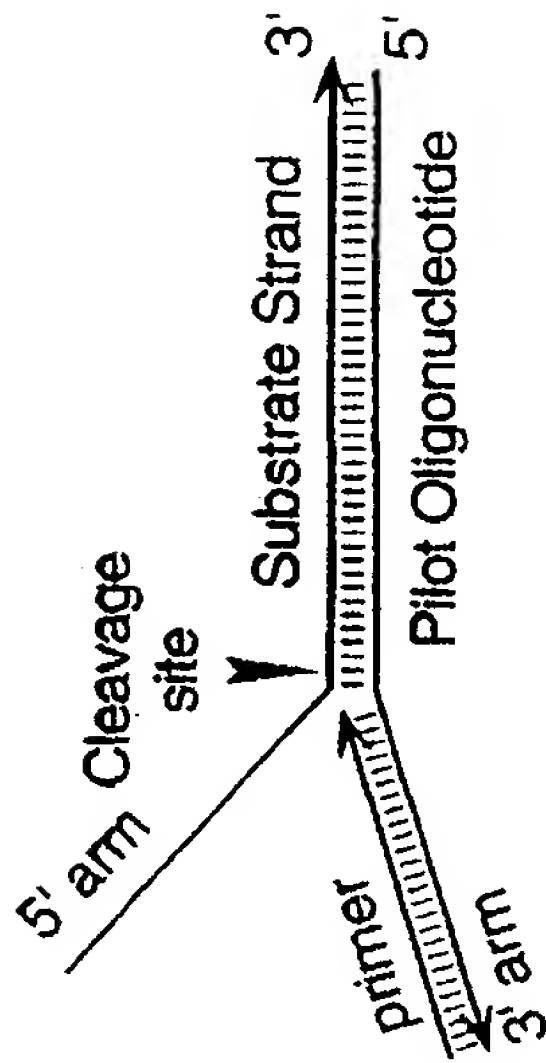


FIG. 16B

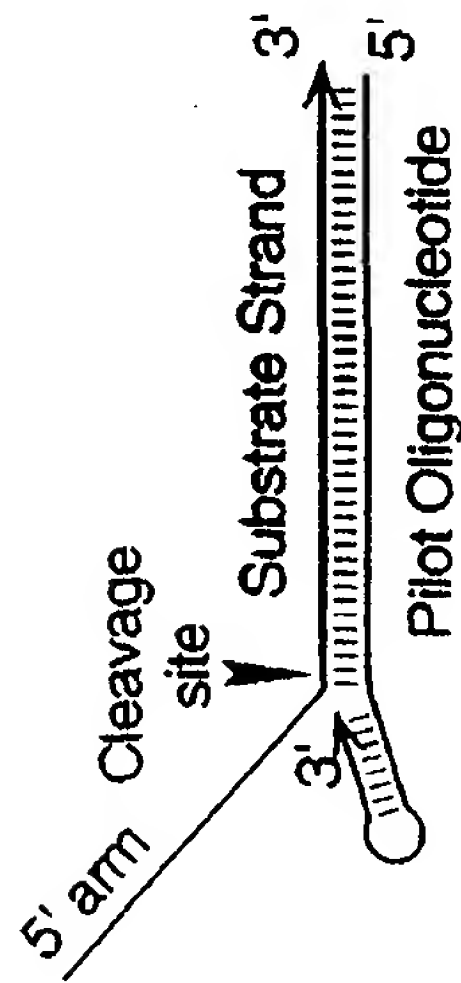


FIG. 16C

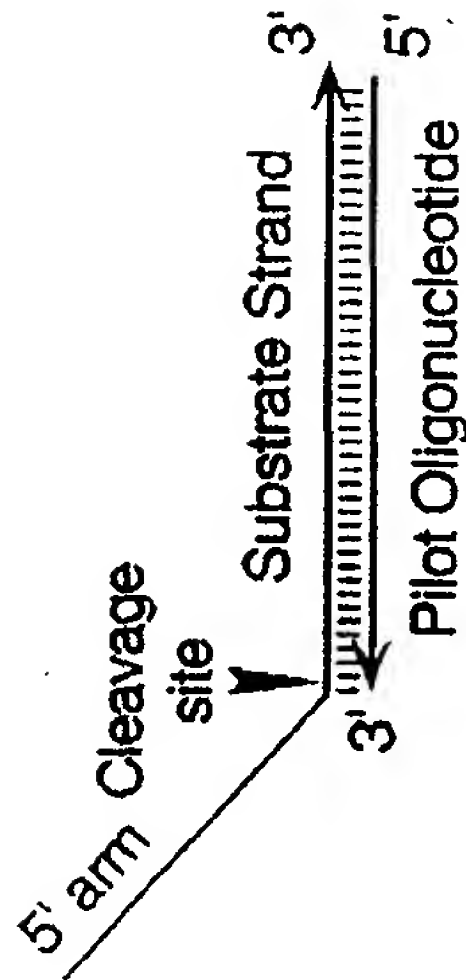


FIG. 16D

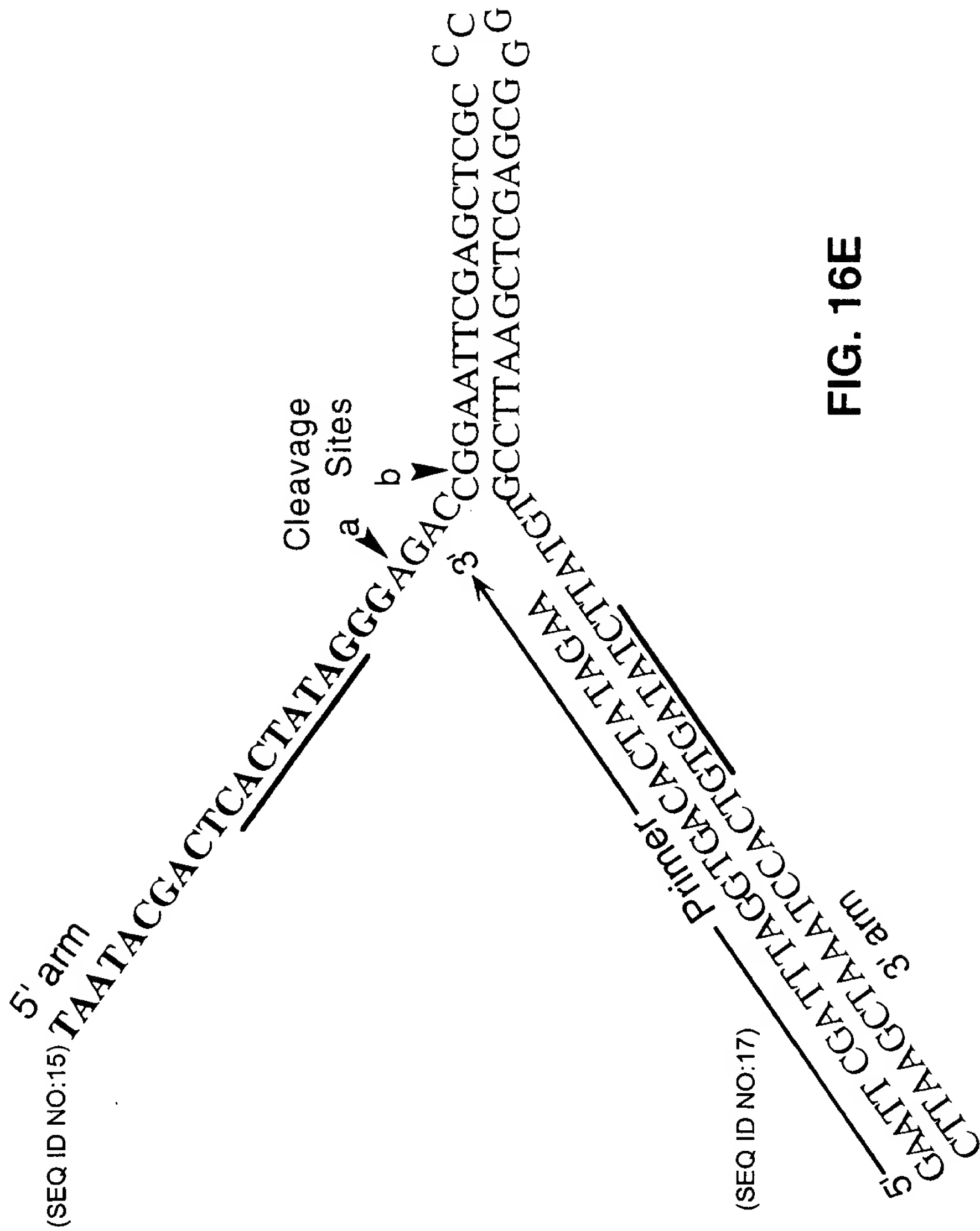
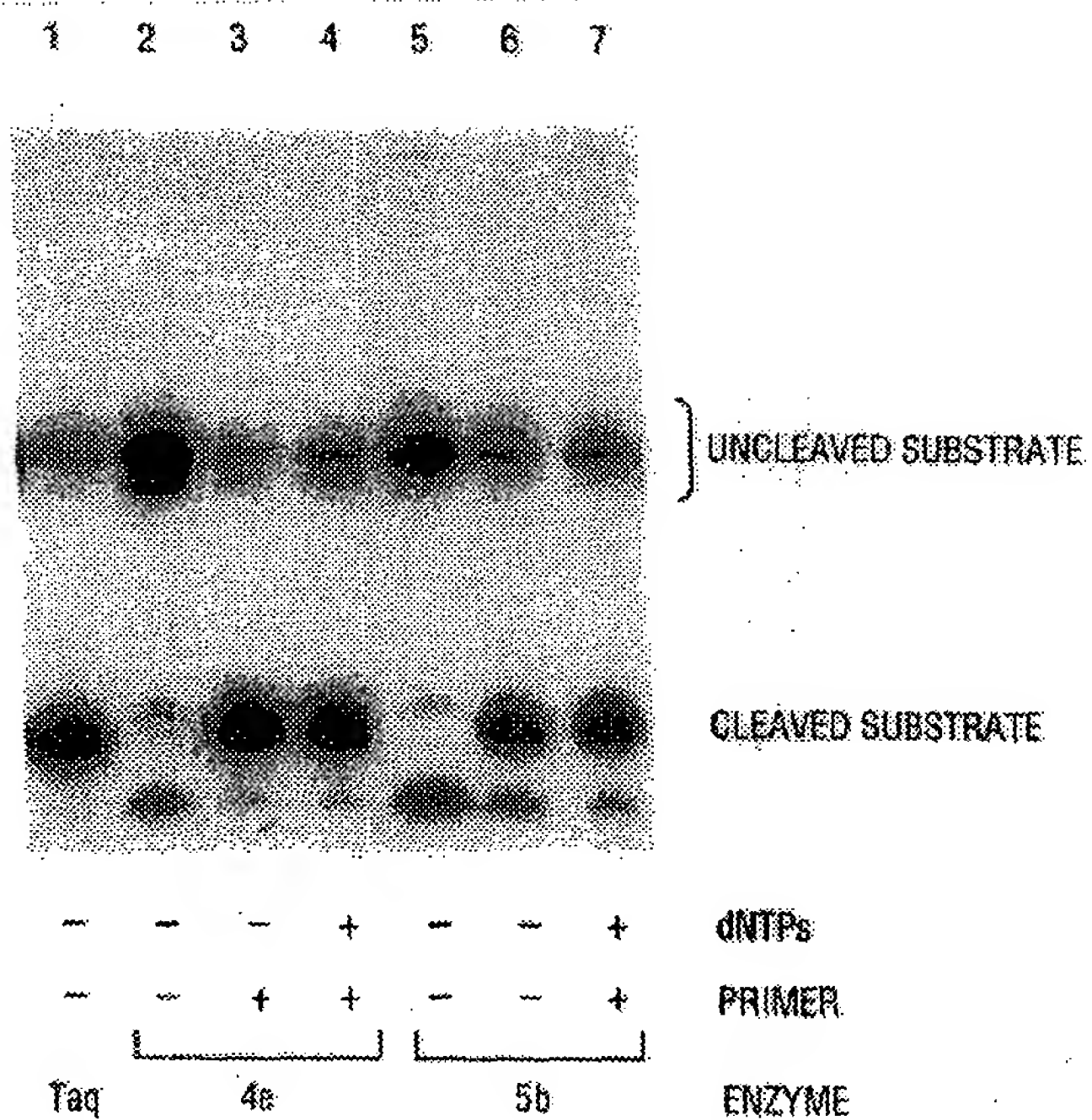


FIG. 16E

FIG. 17



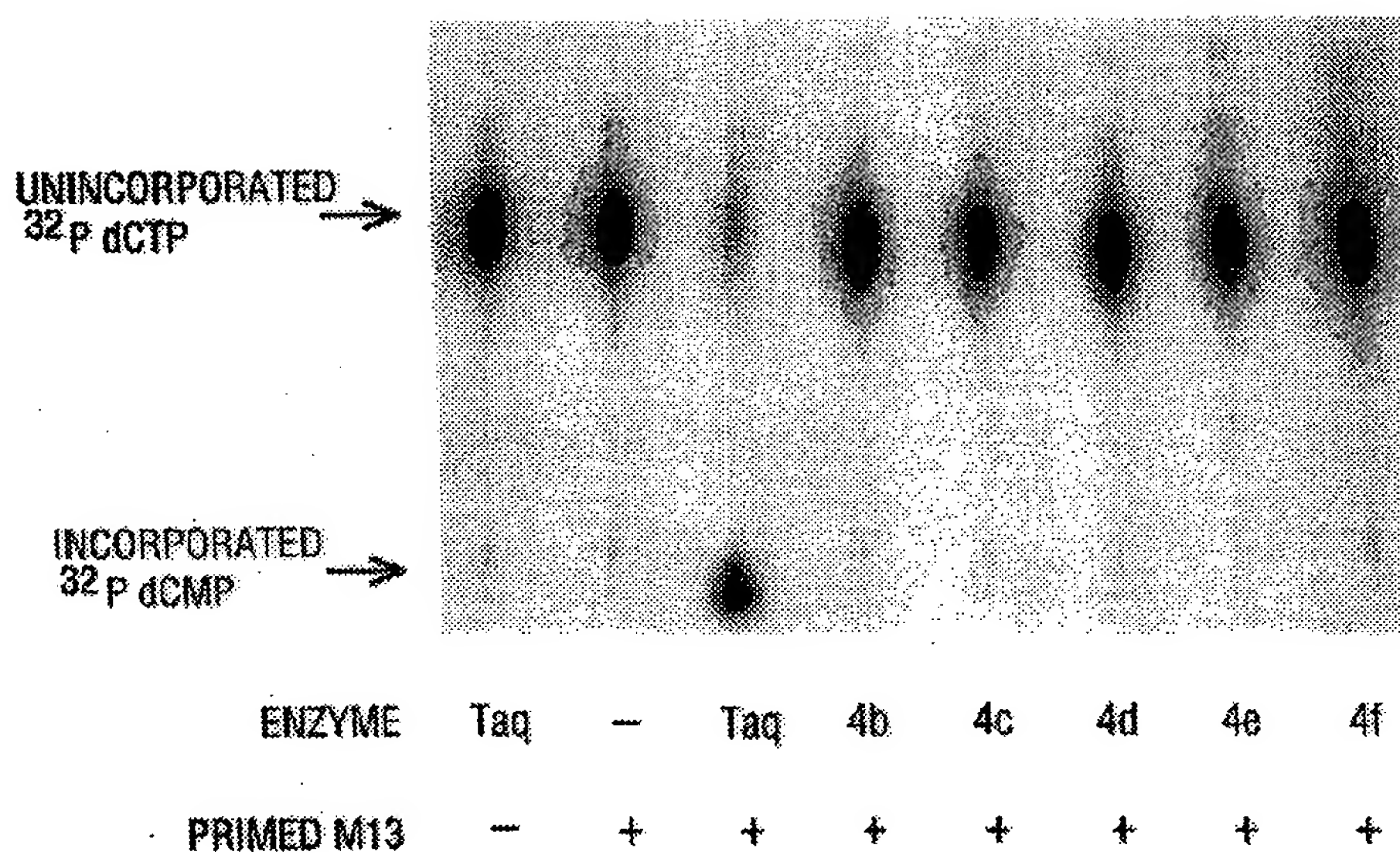


FIG. 18

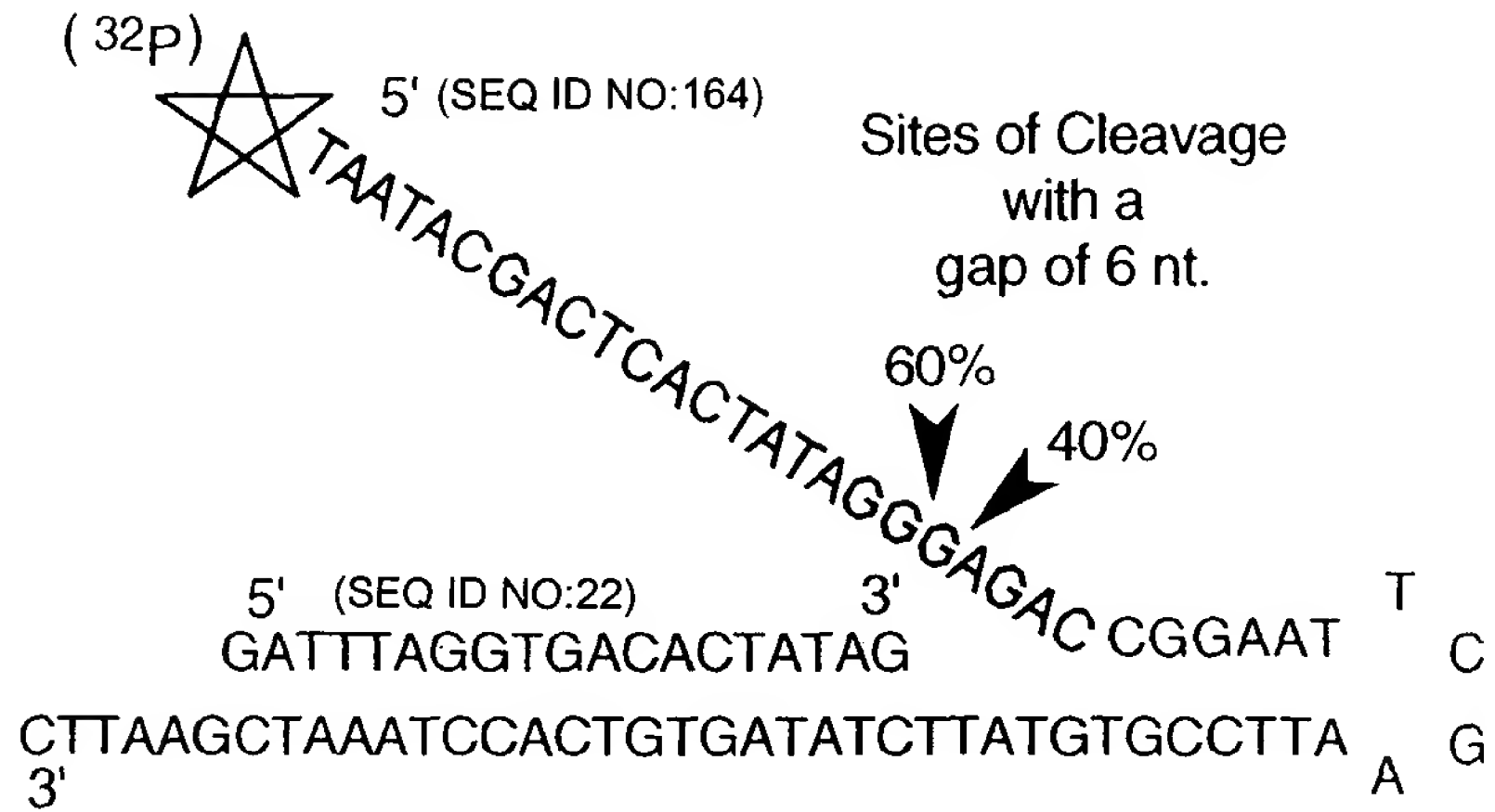


FIG. 19A

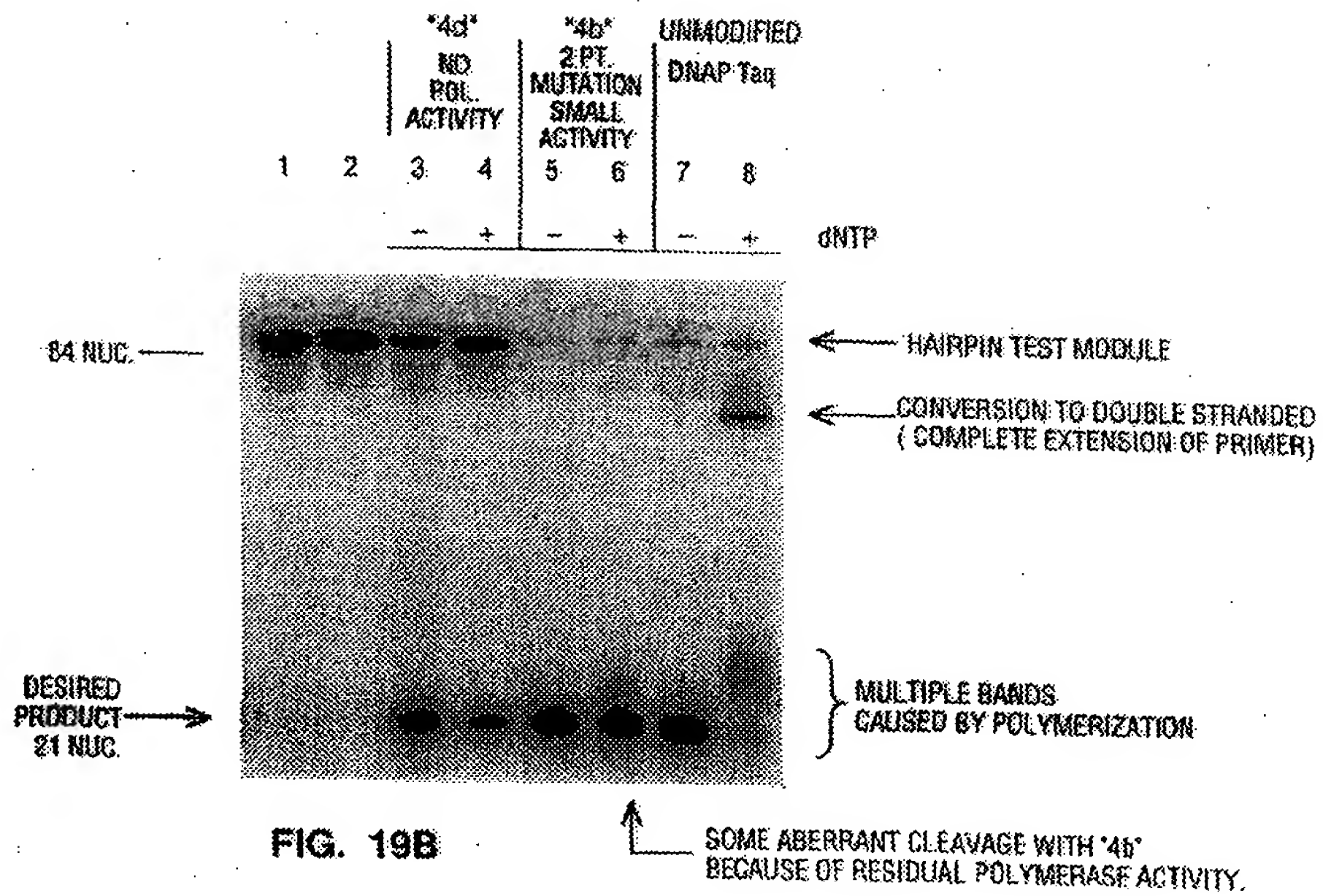


FIG. 19B



FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)

FIG. 20B

FIG. 20C

(SEQ ID NO:28)

FIG. 20D

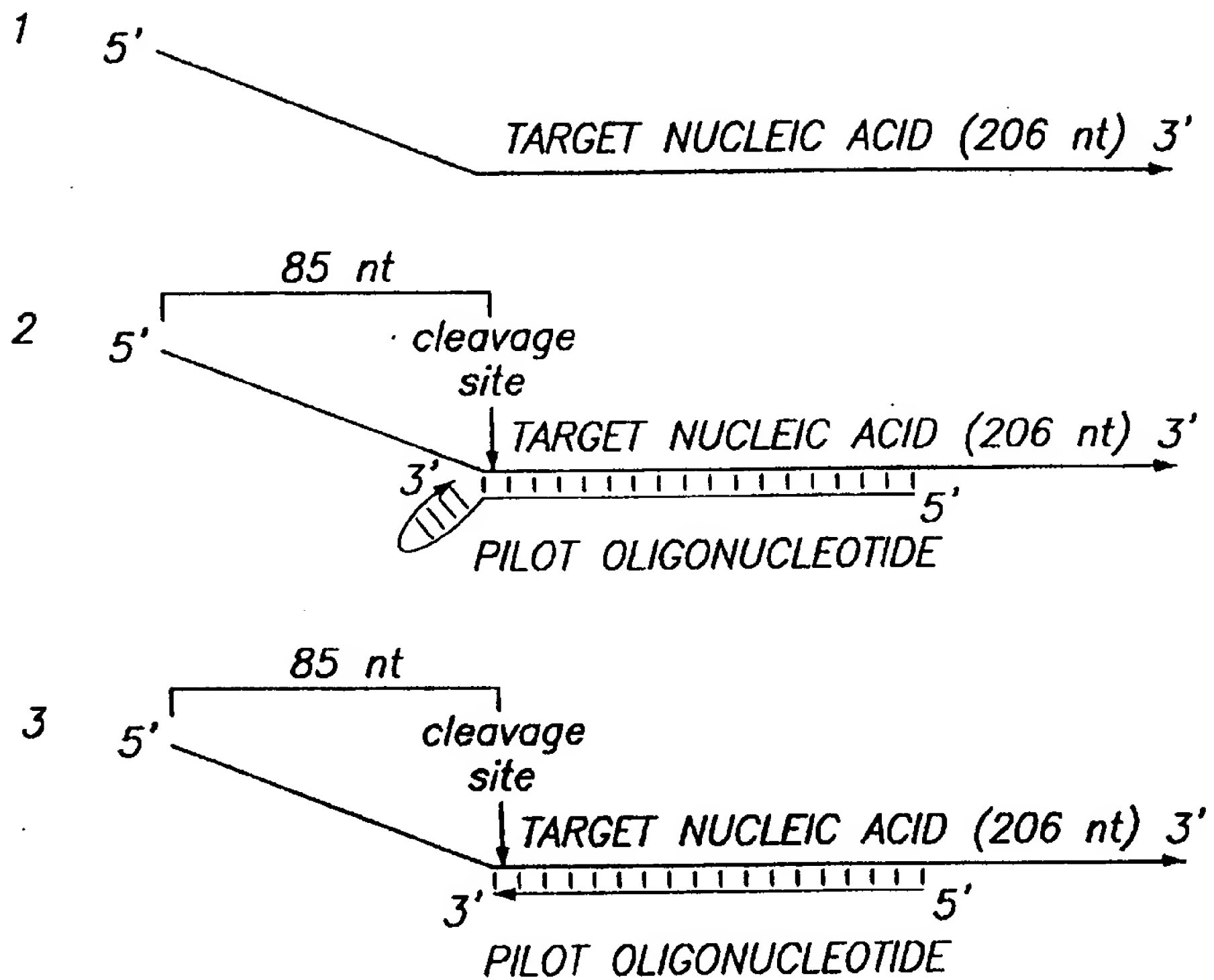
09940925, 061002

TCCGCTCACAATTCCACACACAACATACGA  
 AGCGGAGTGTAAAGGTGTGTGATGCT

— — 48 Reverse  
 — — 206

228

**FIG. 21**

**FIG. 22A**

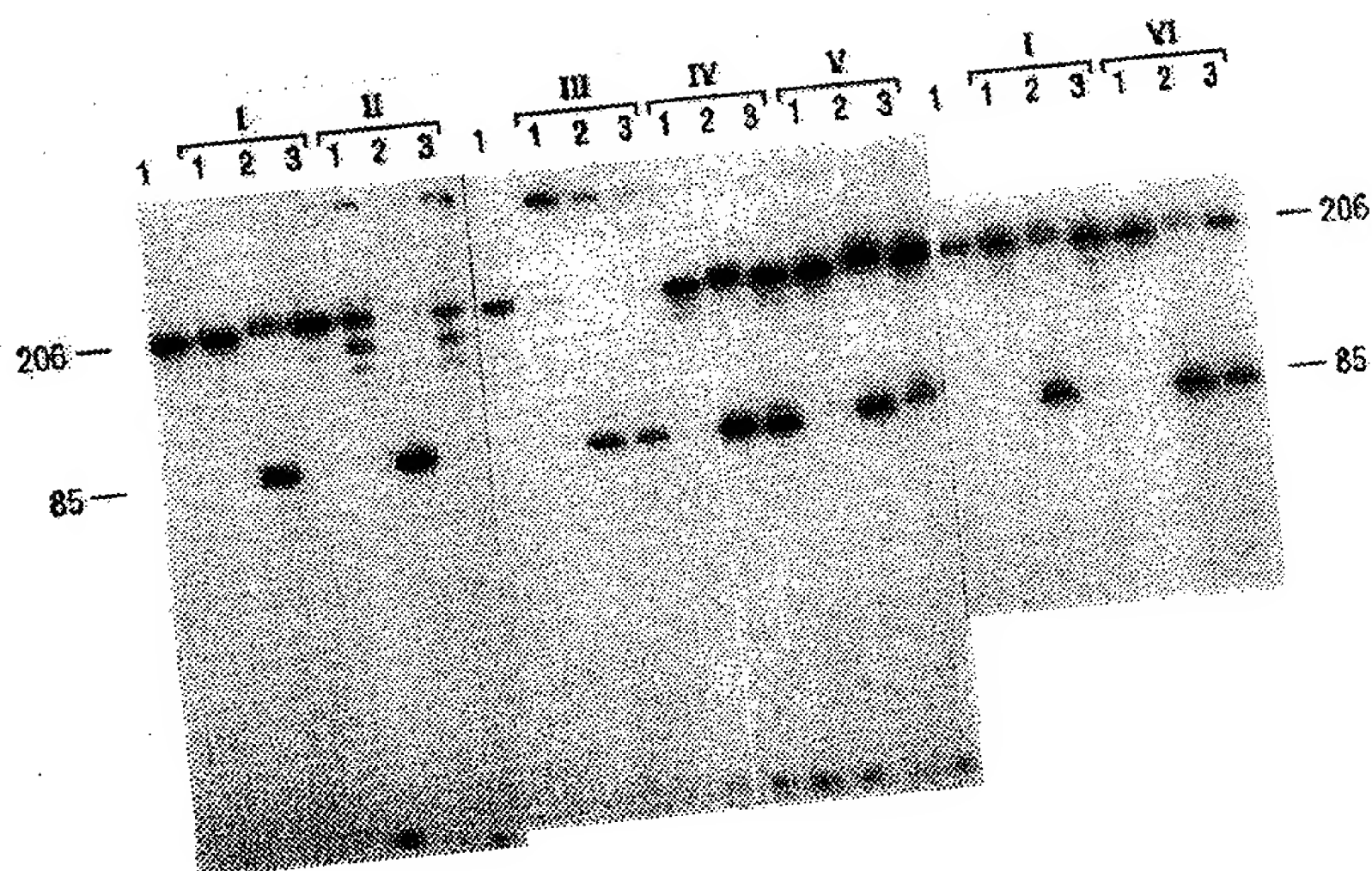


FIG. 22B

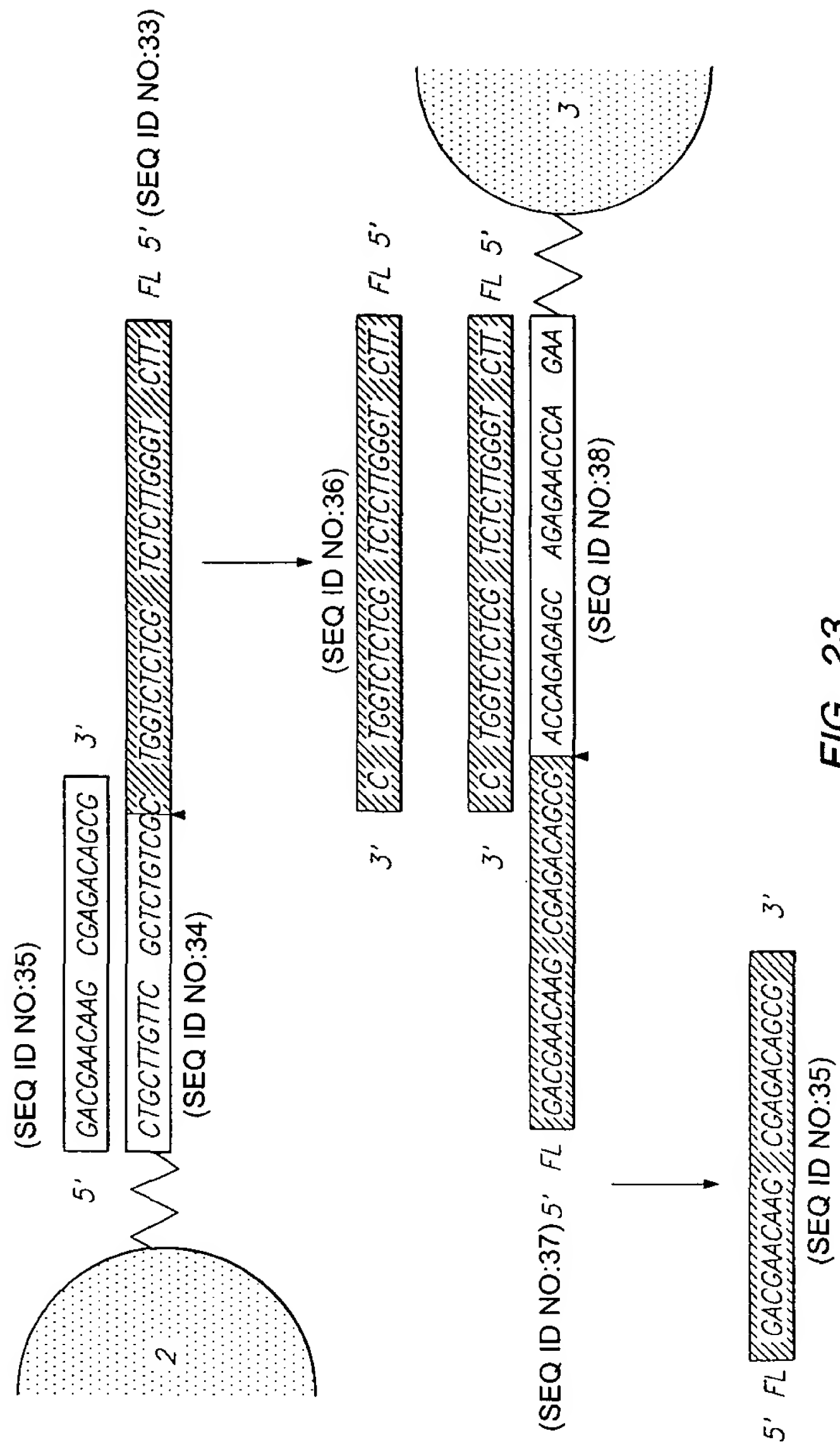


FIG. 23

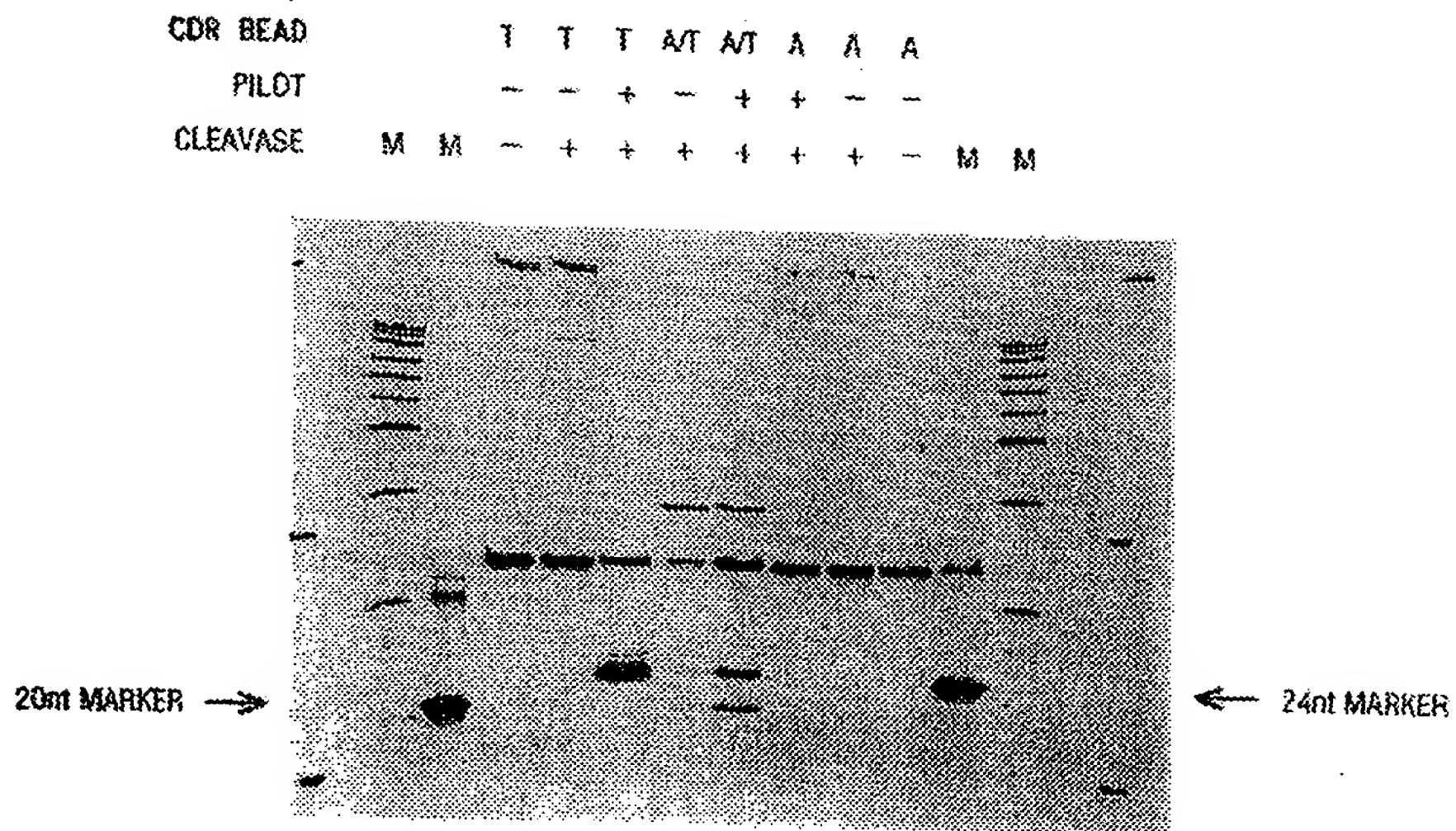


FIG. 24

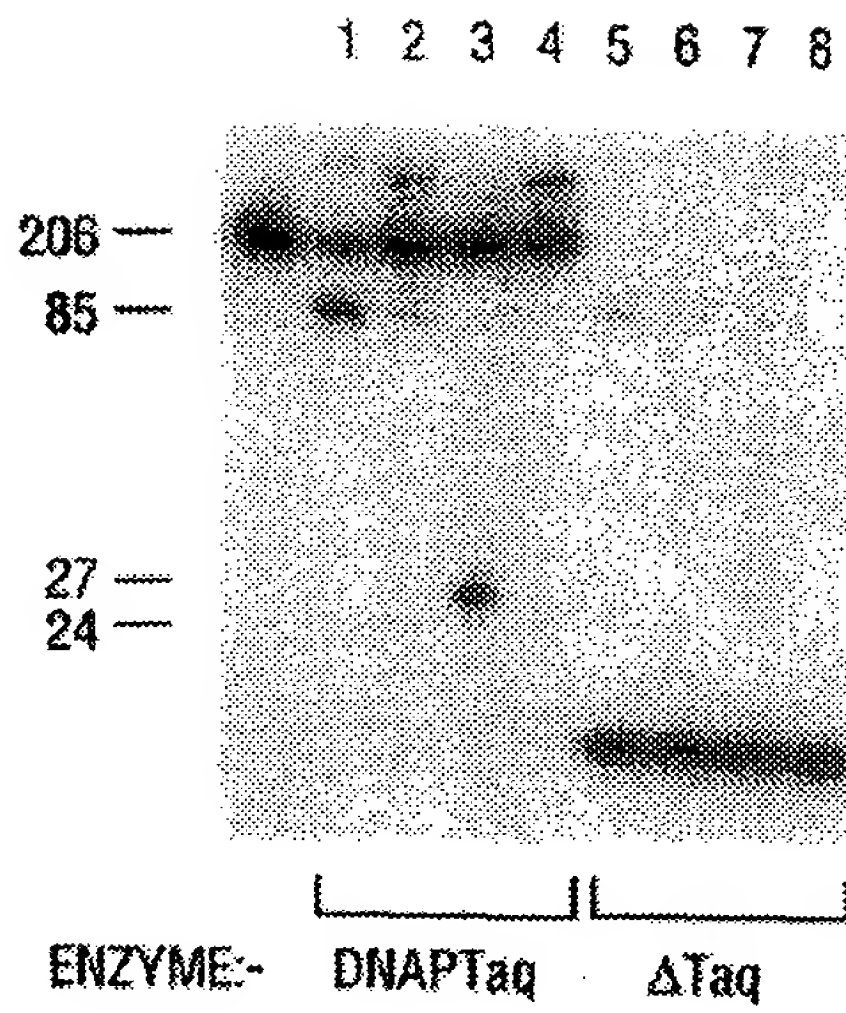


FIG. 25A

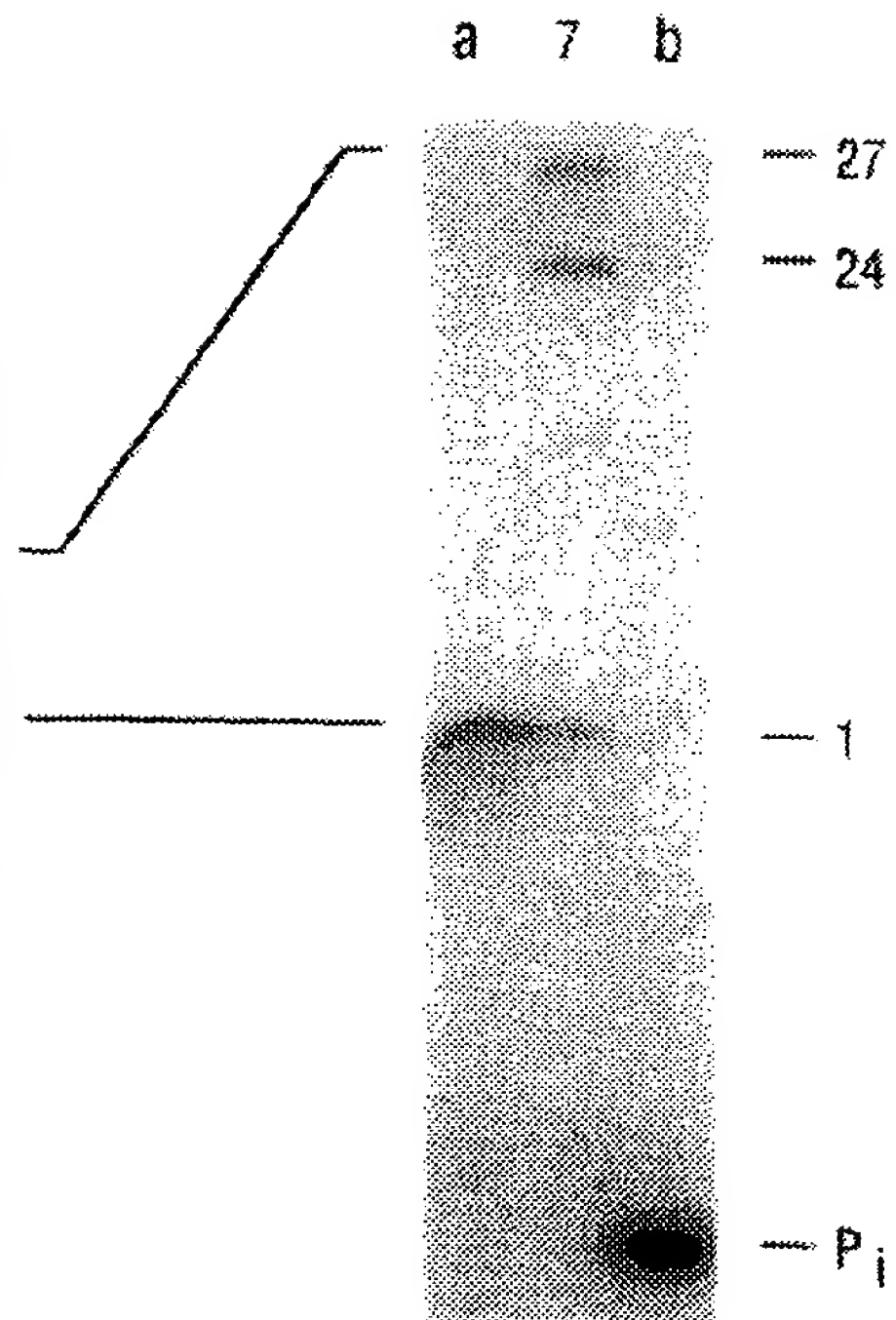


FIG. 25B

FIG. 26A

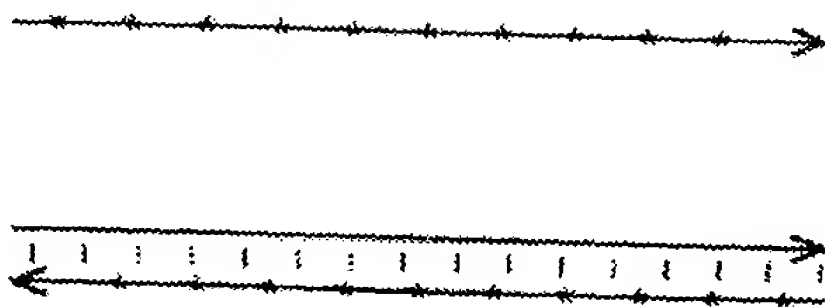
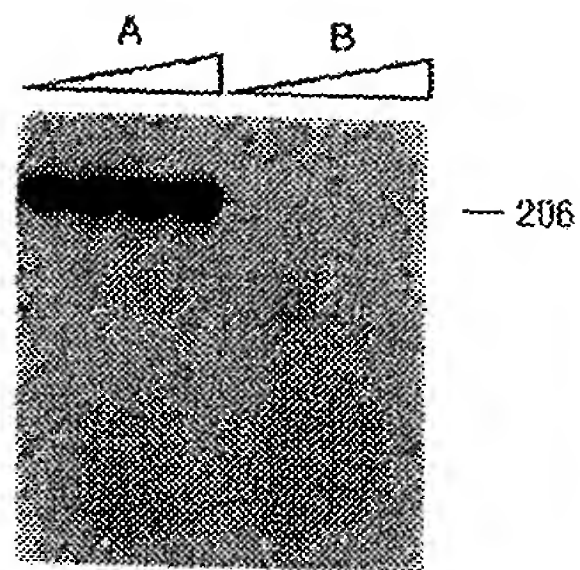


FIG. 26B

$\star = 32p$





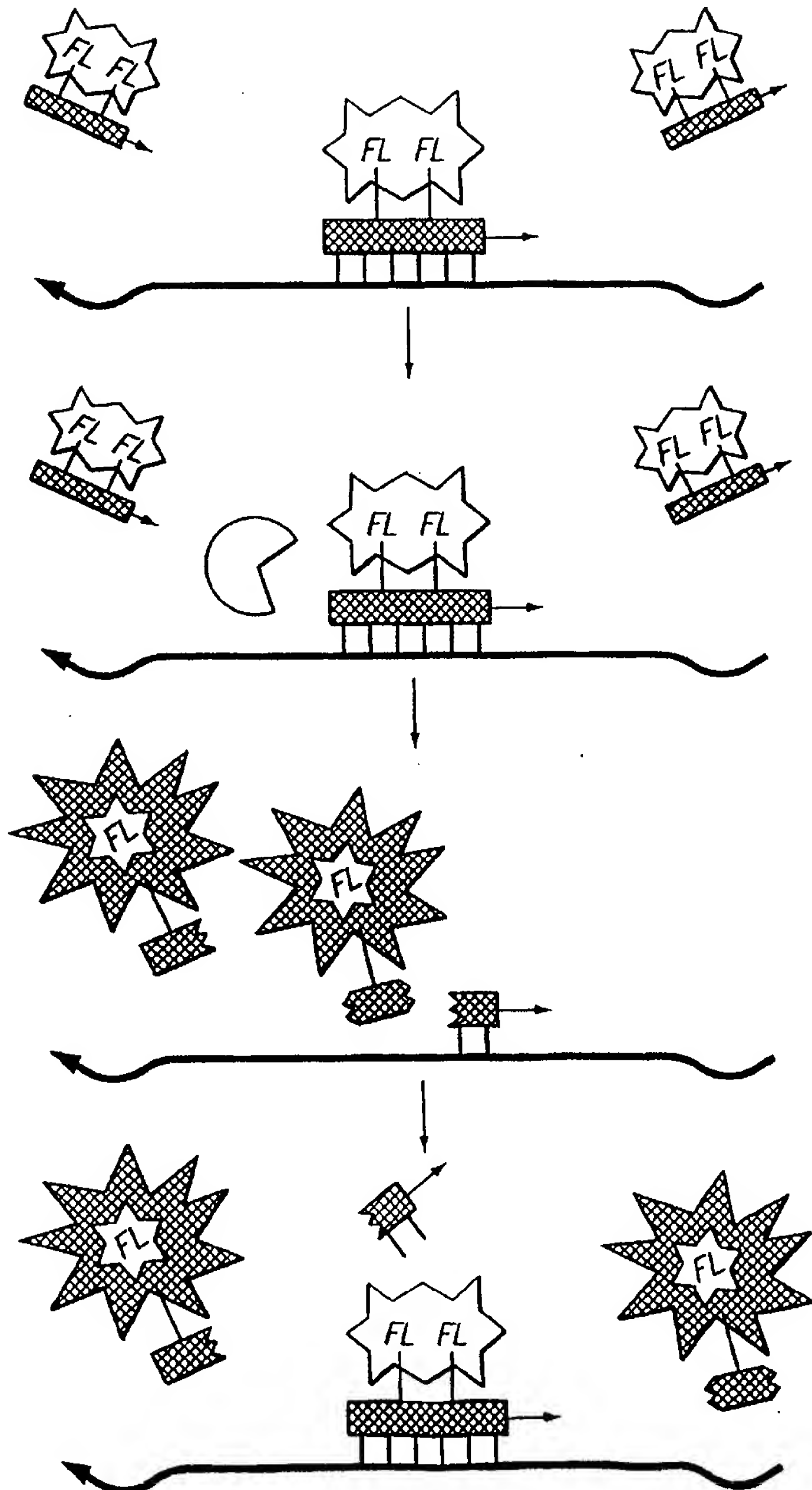
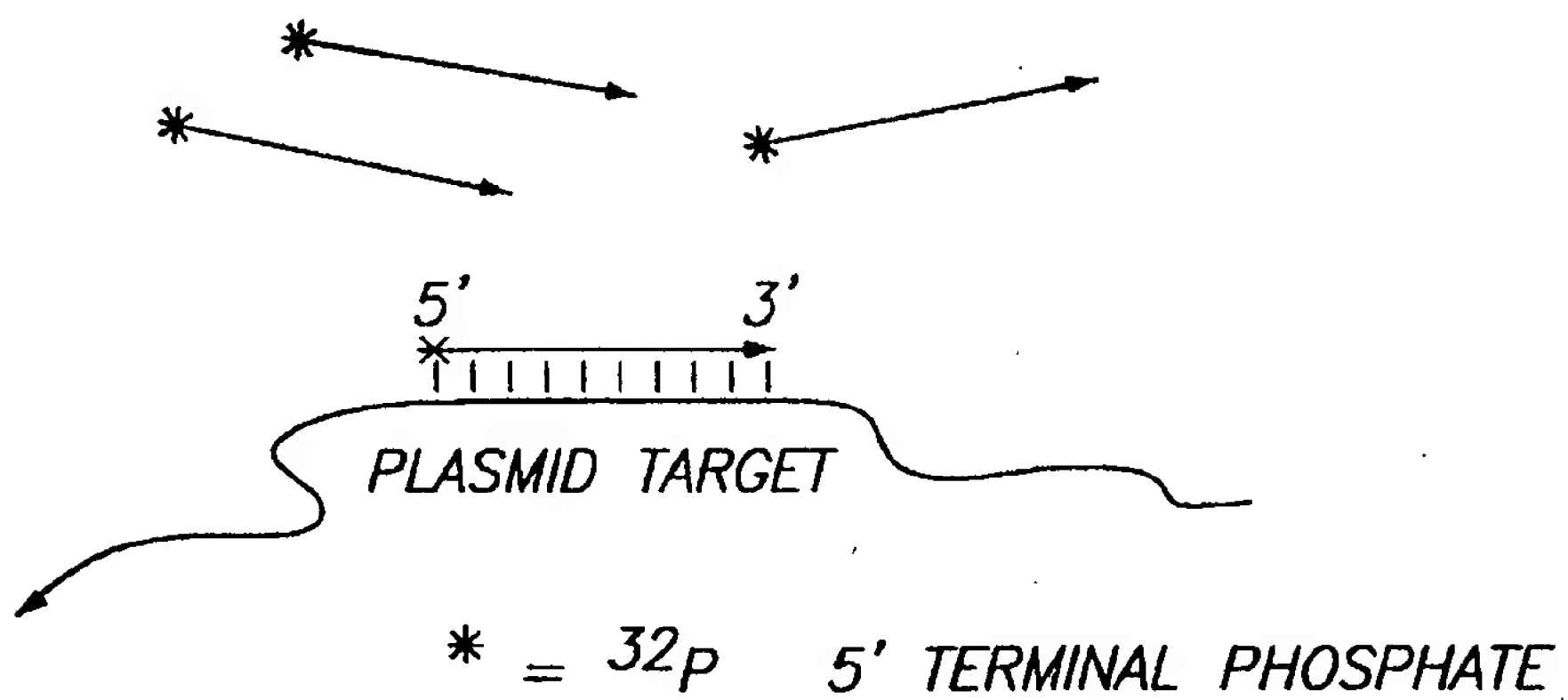
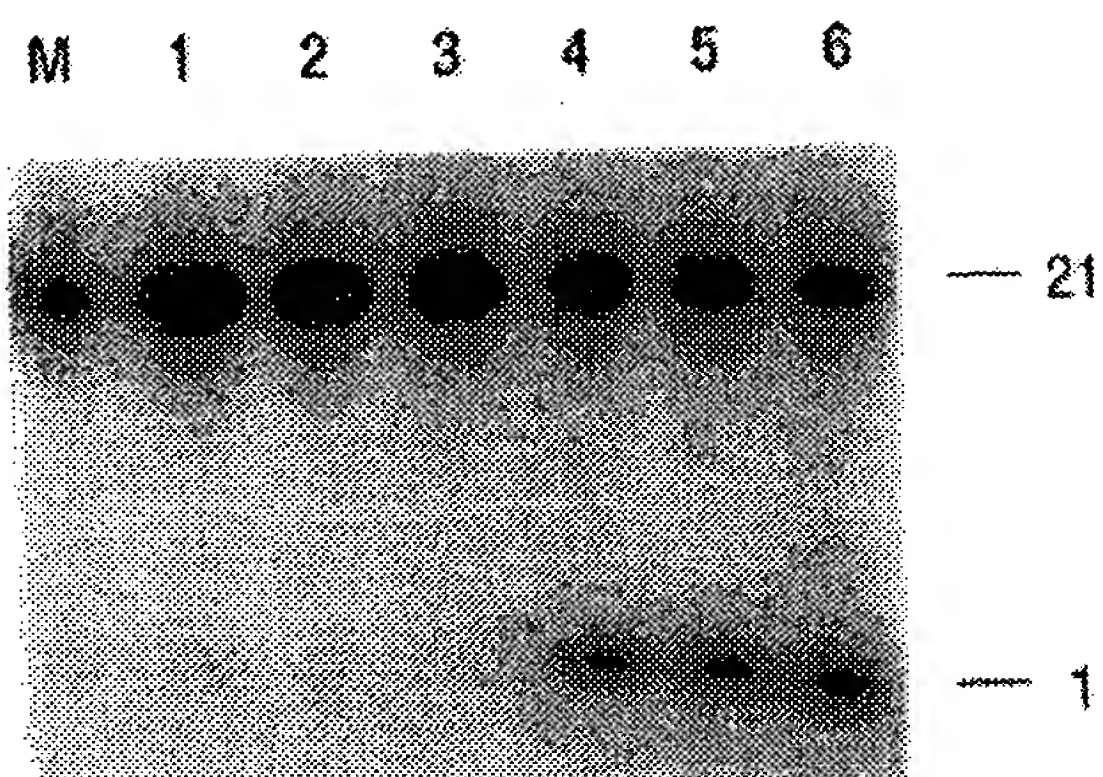
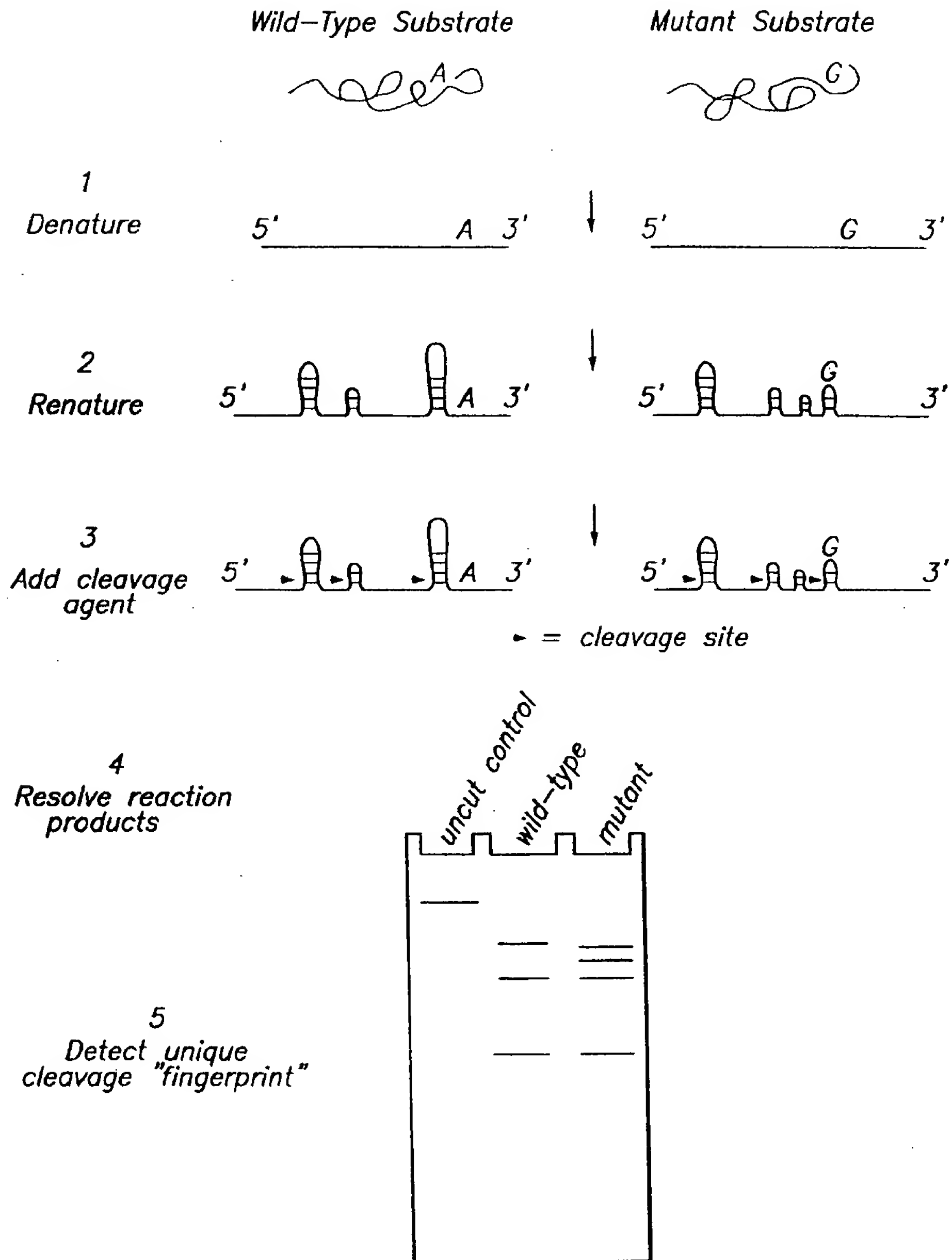
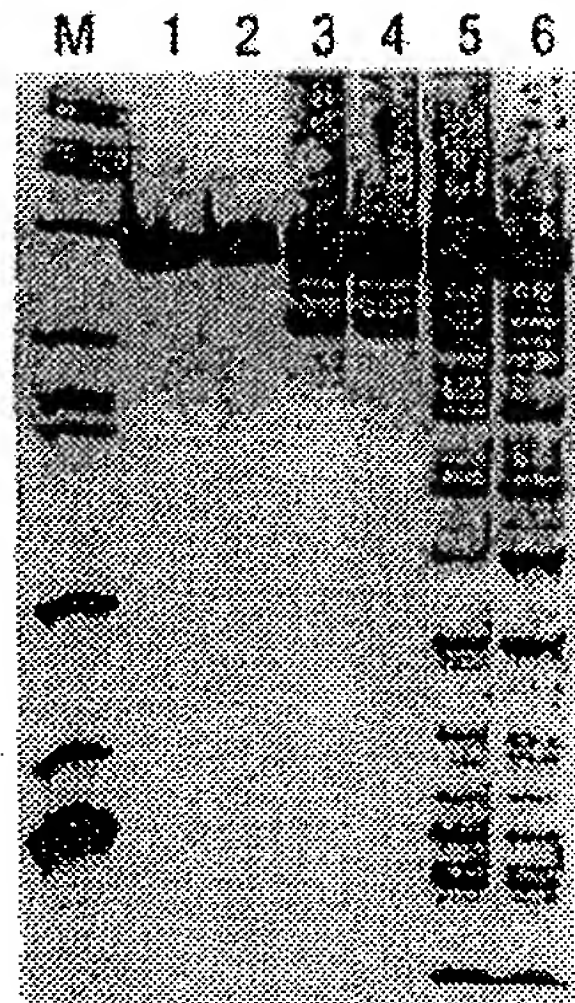


FIG. 27

**FIG. 28A**

**FIG. 28B**

**FIG. 29**

**FIG. 30**

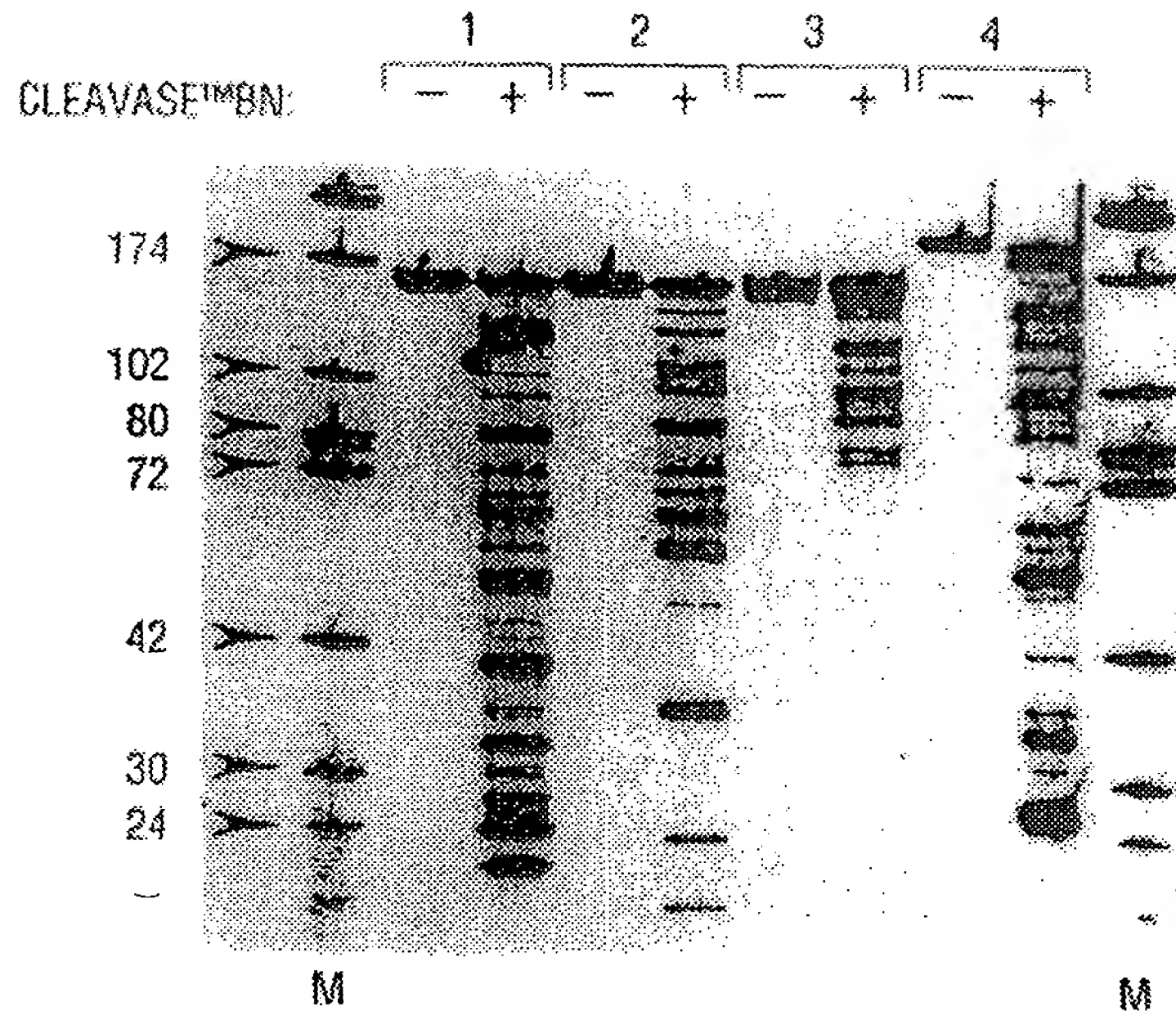


FIG. 31

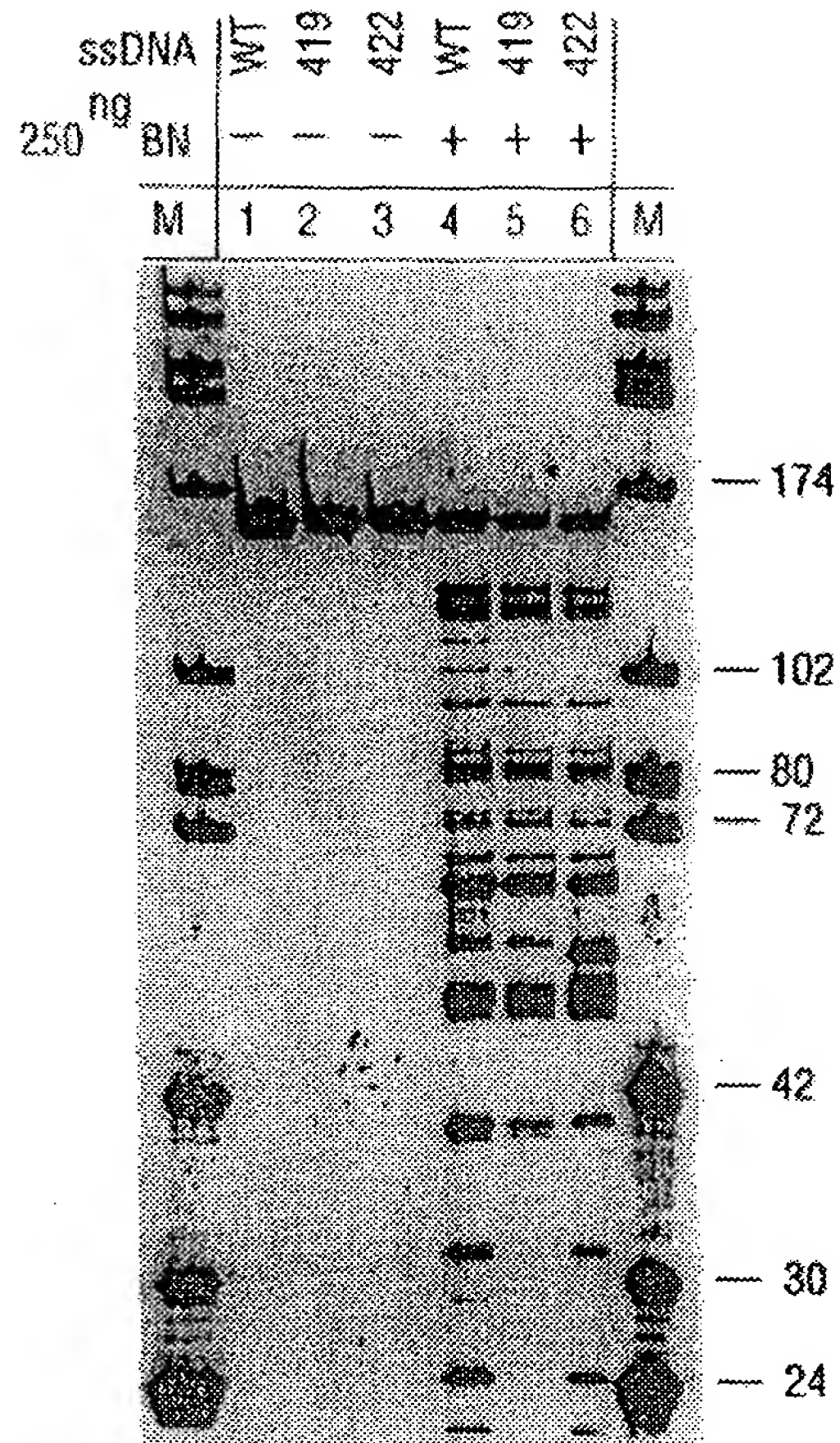


FIG. 32

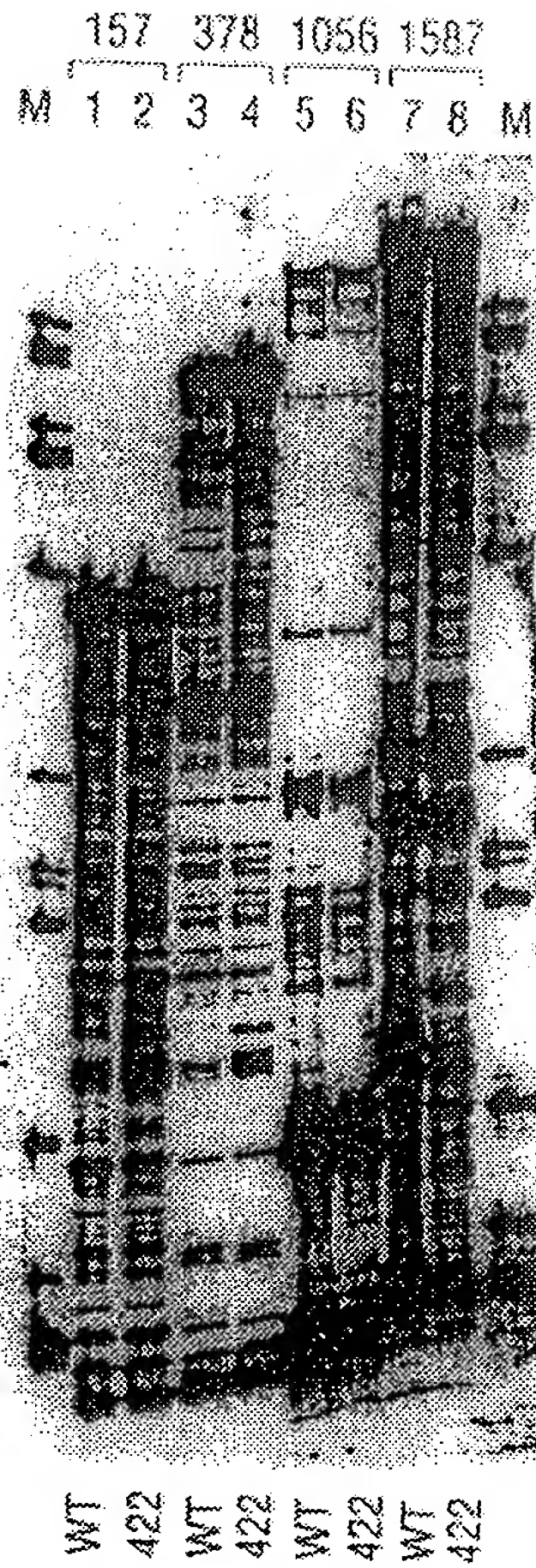


FIG. 33



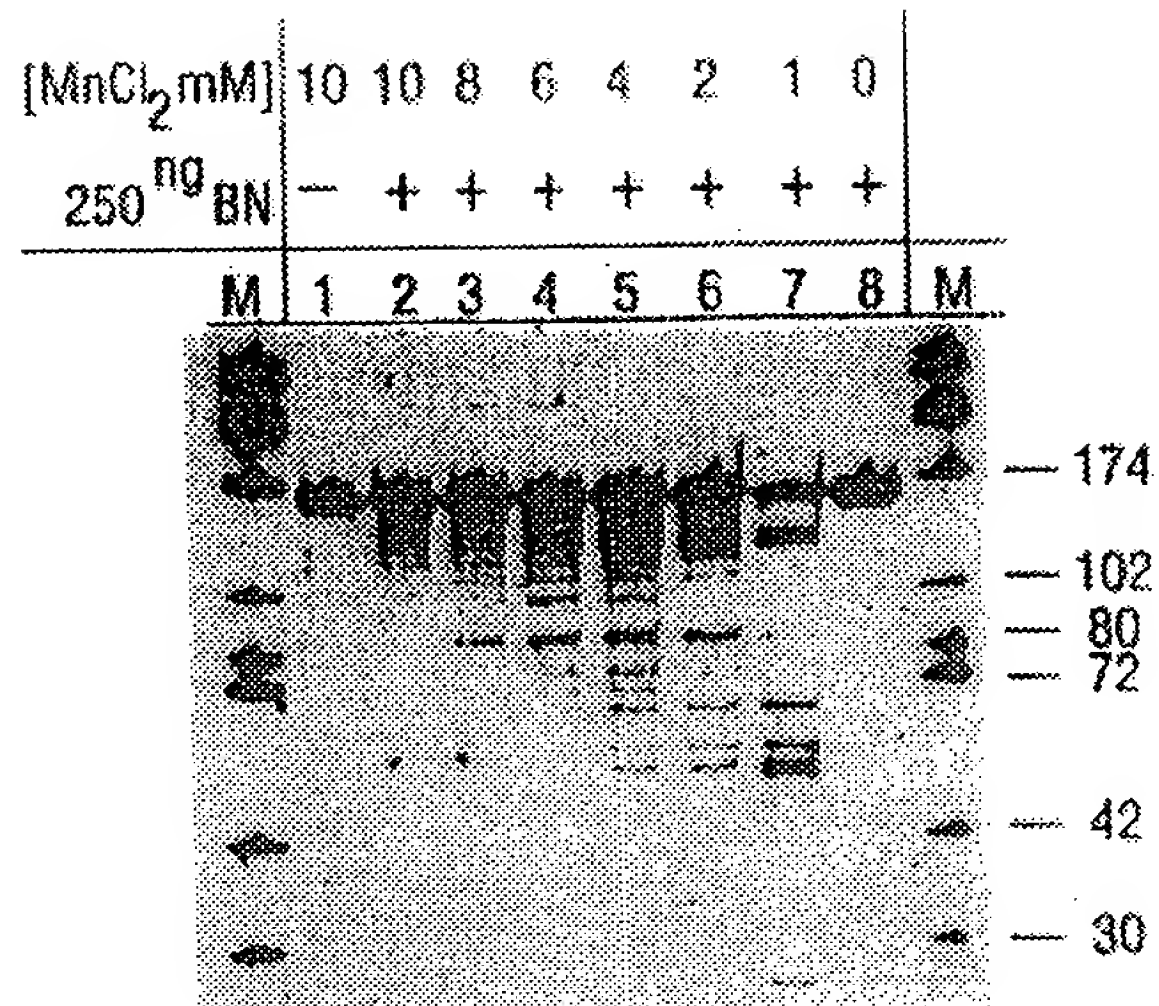


FIG. 34

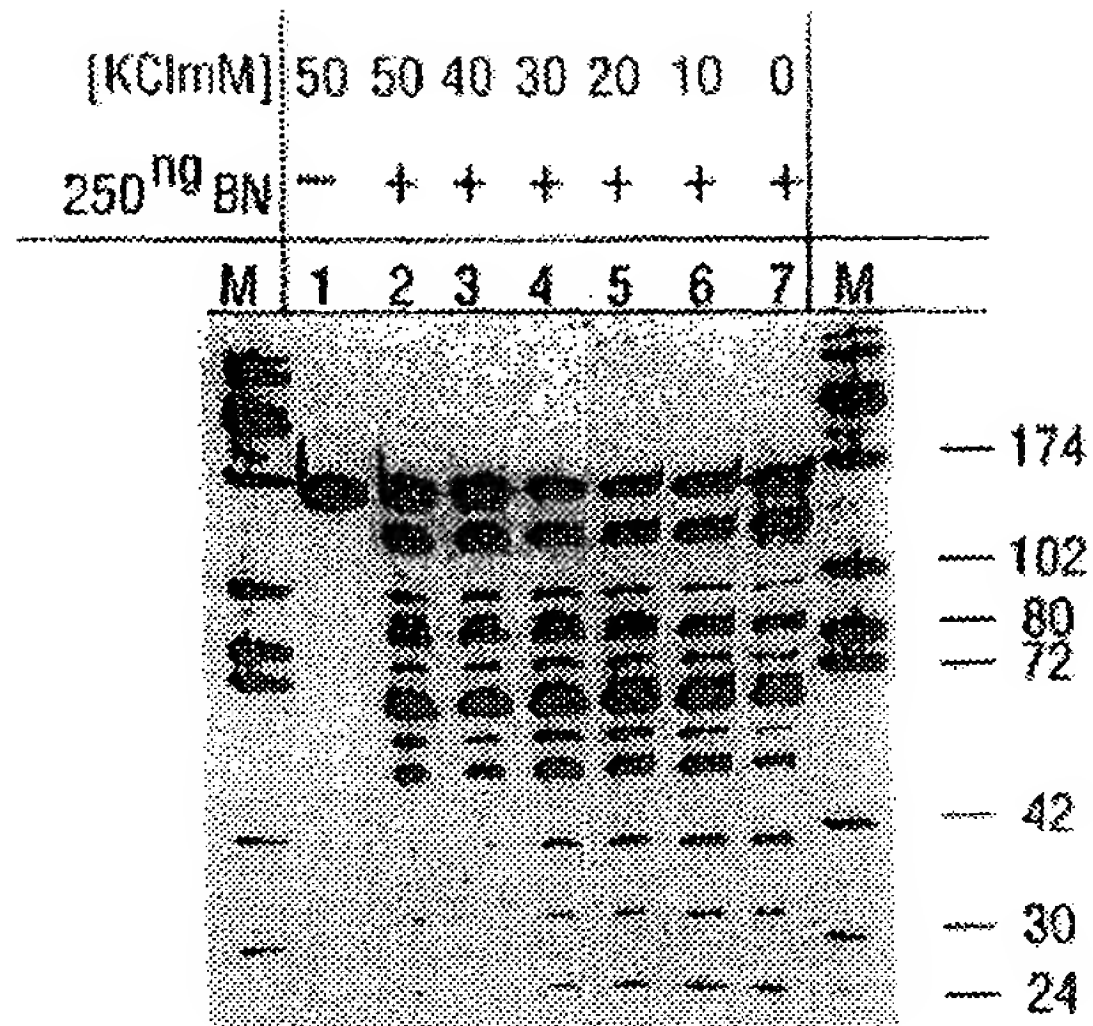


FIG. 35

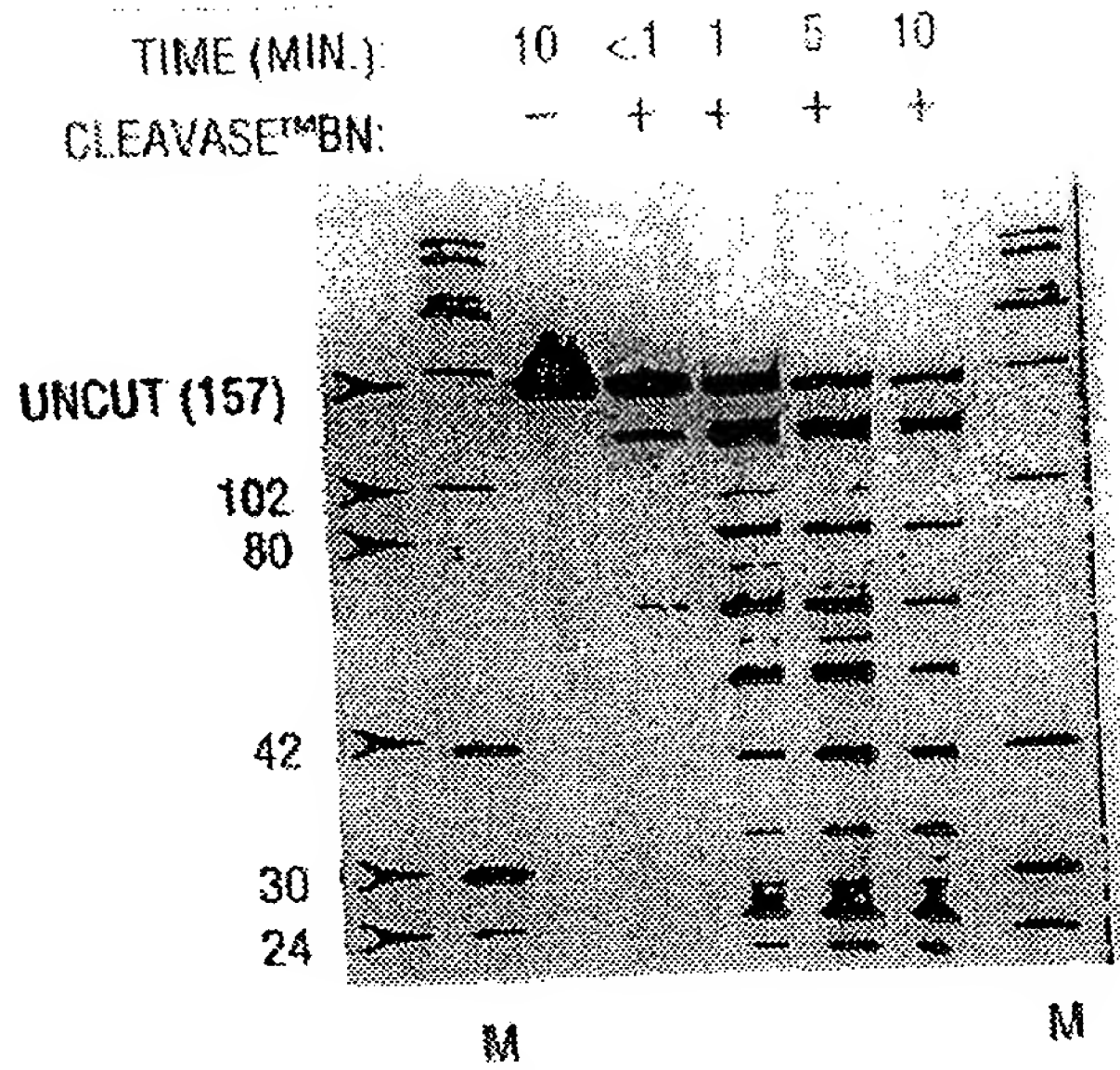


FIG. 36

TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	—	—	+	+	+	+	—	+

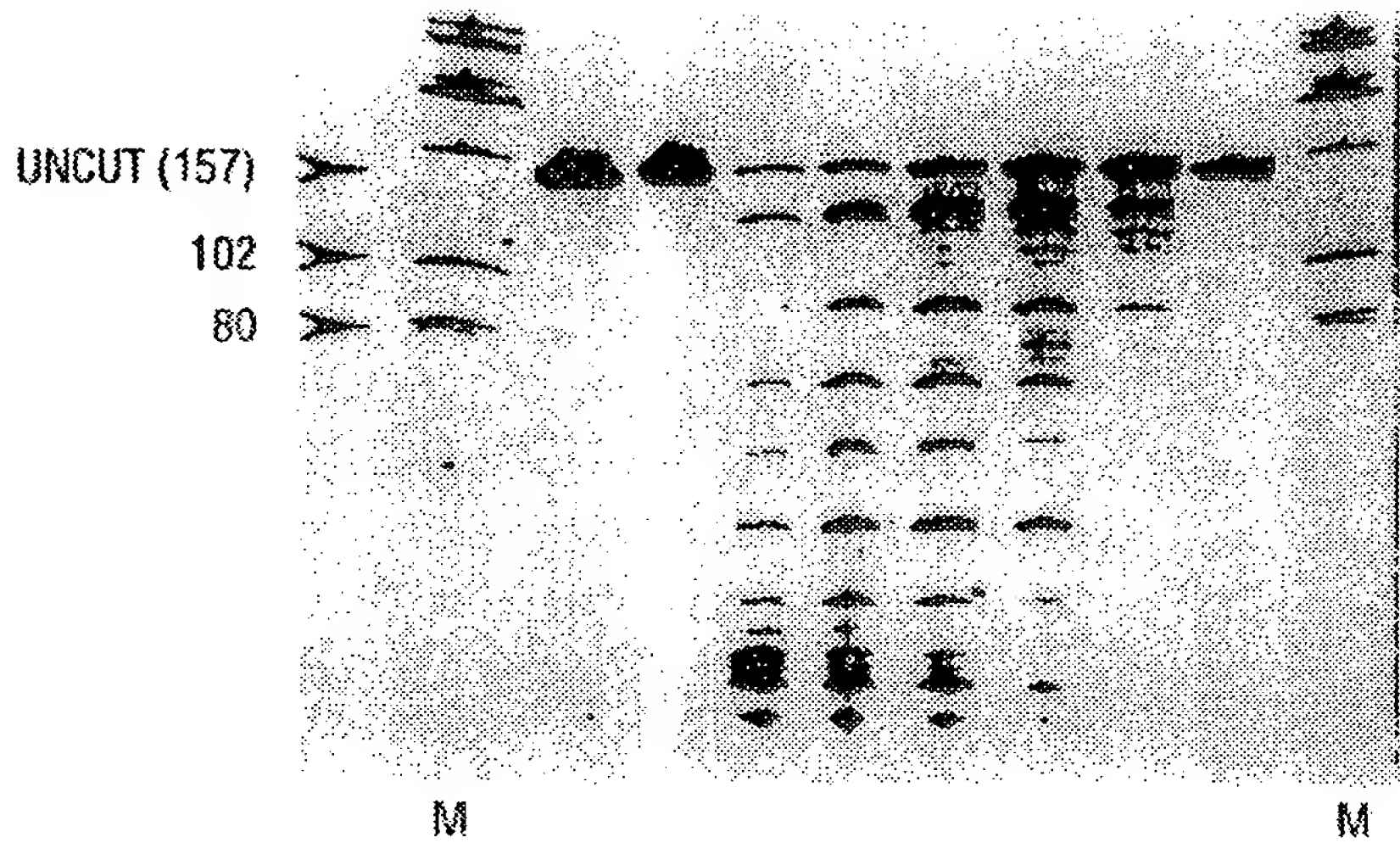


FIG. 37

CLEAVASE™BN (ng): — 10 50 100 250

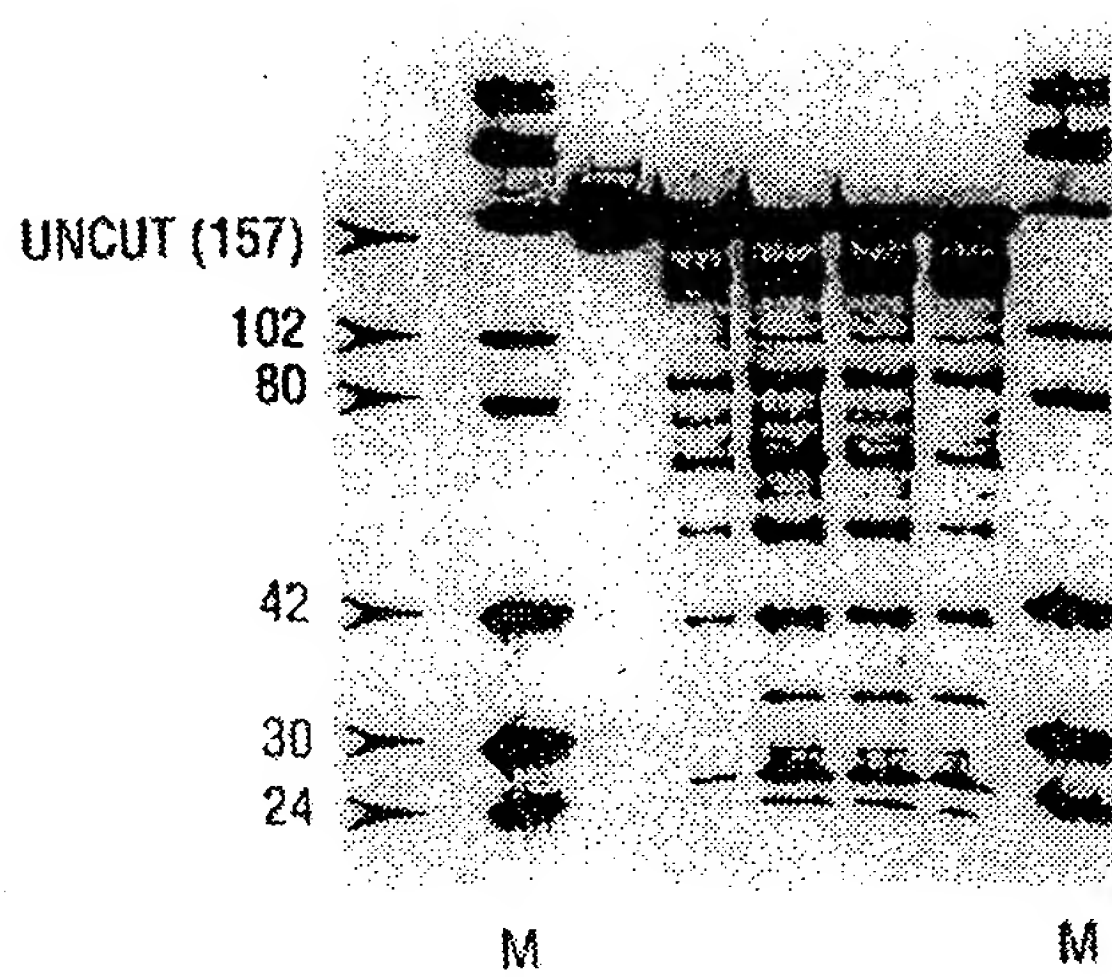


FIG. 38

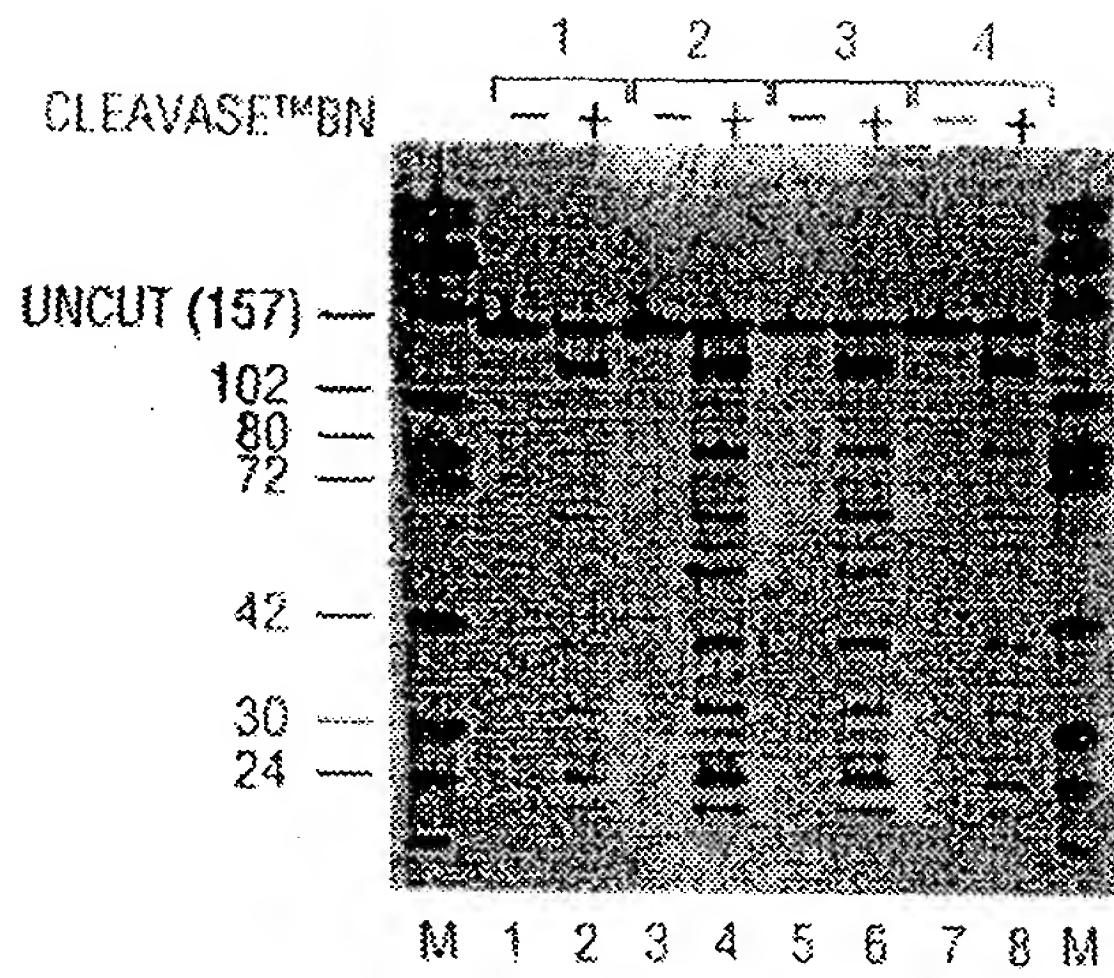


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

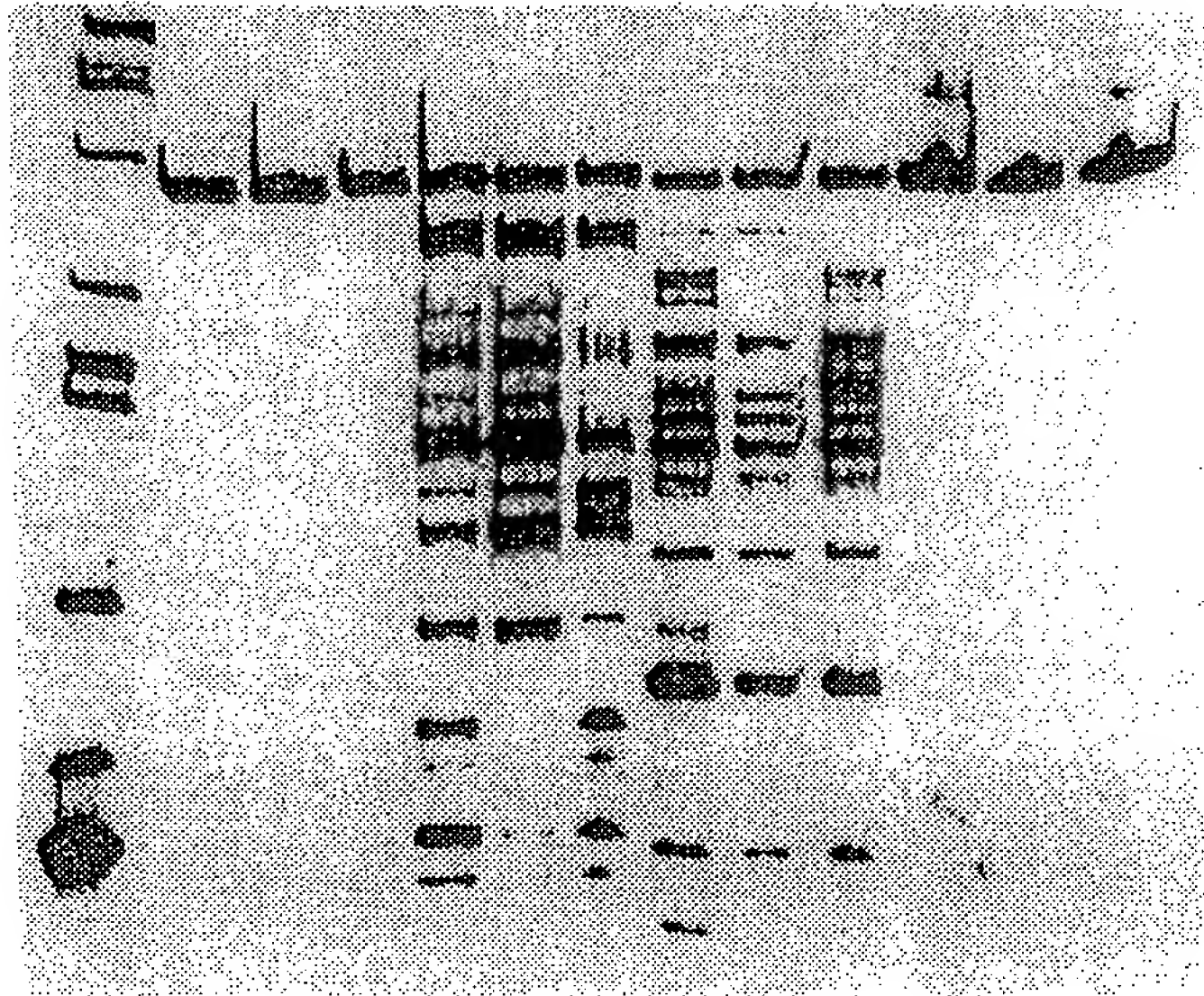


FIG. 40



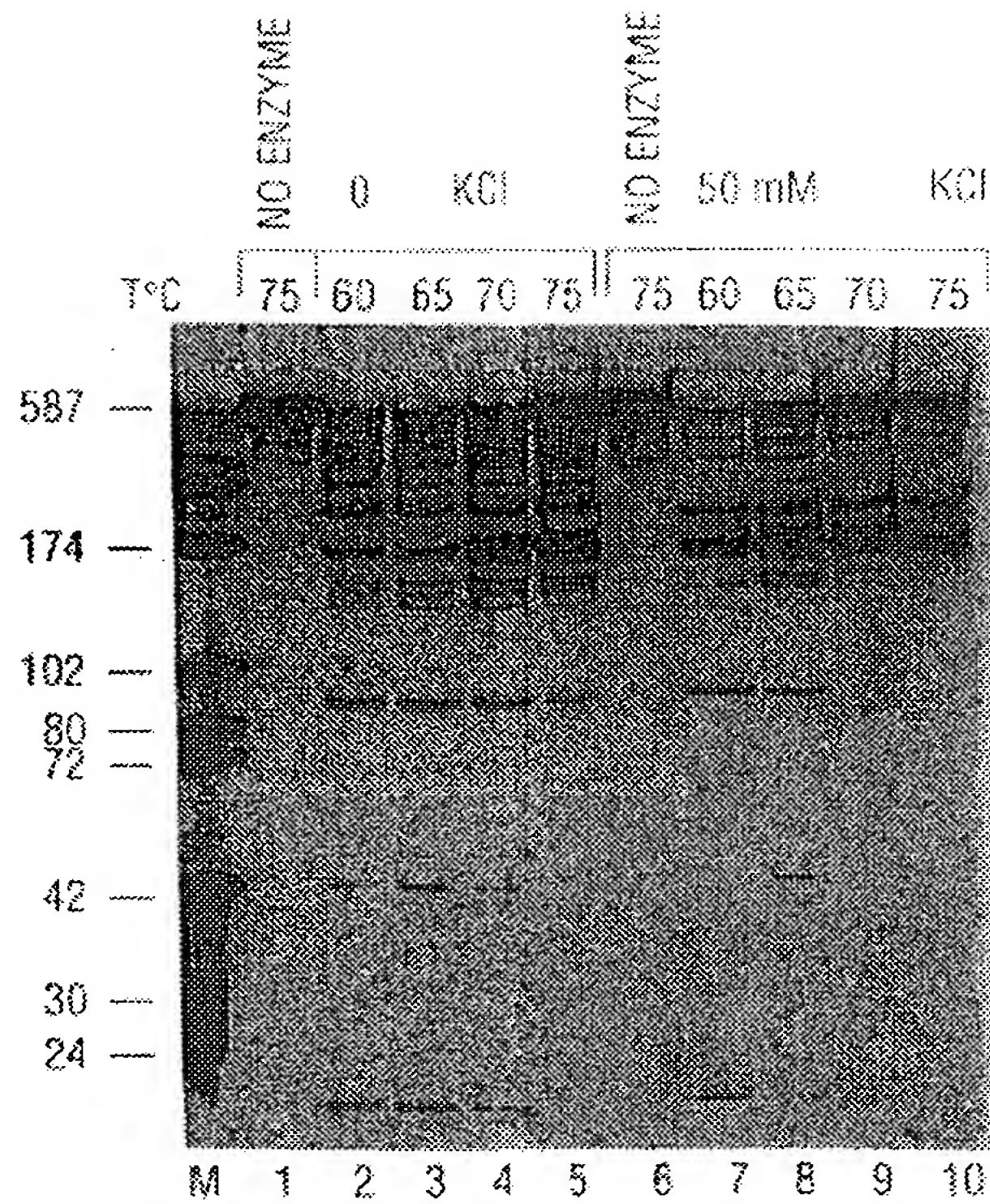


FIG. 41



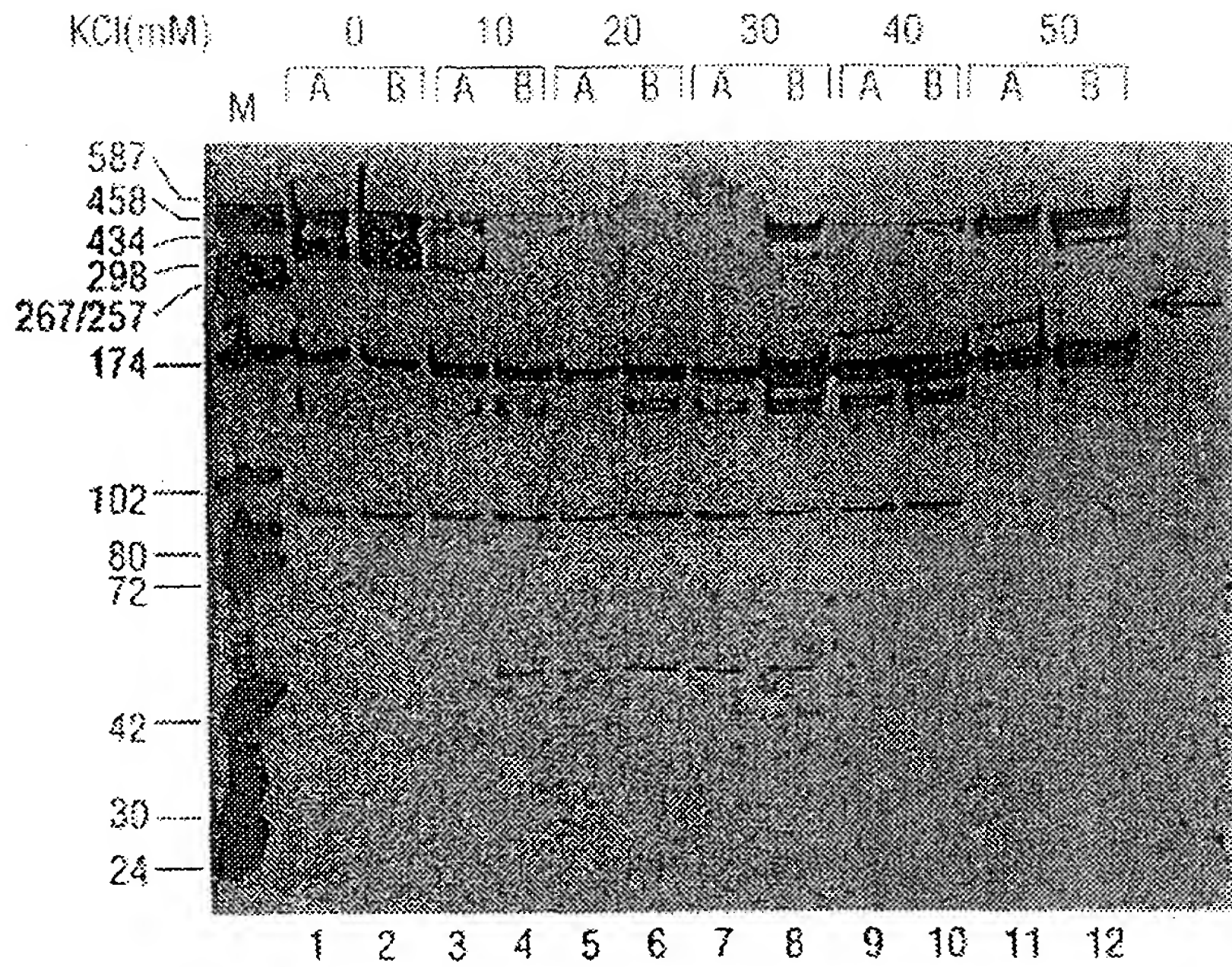


FIG. 42

CLEAVASE™BN

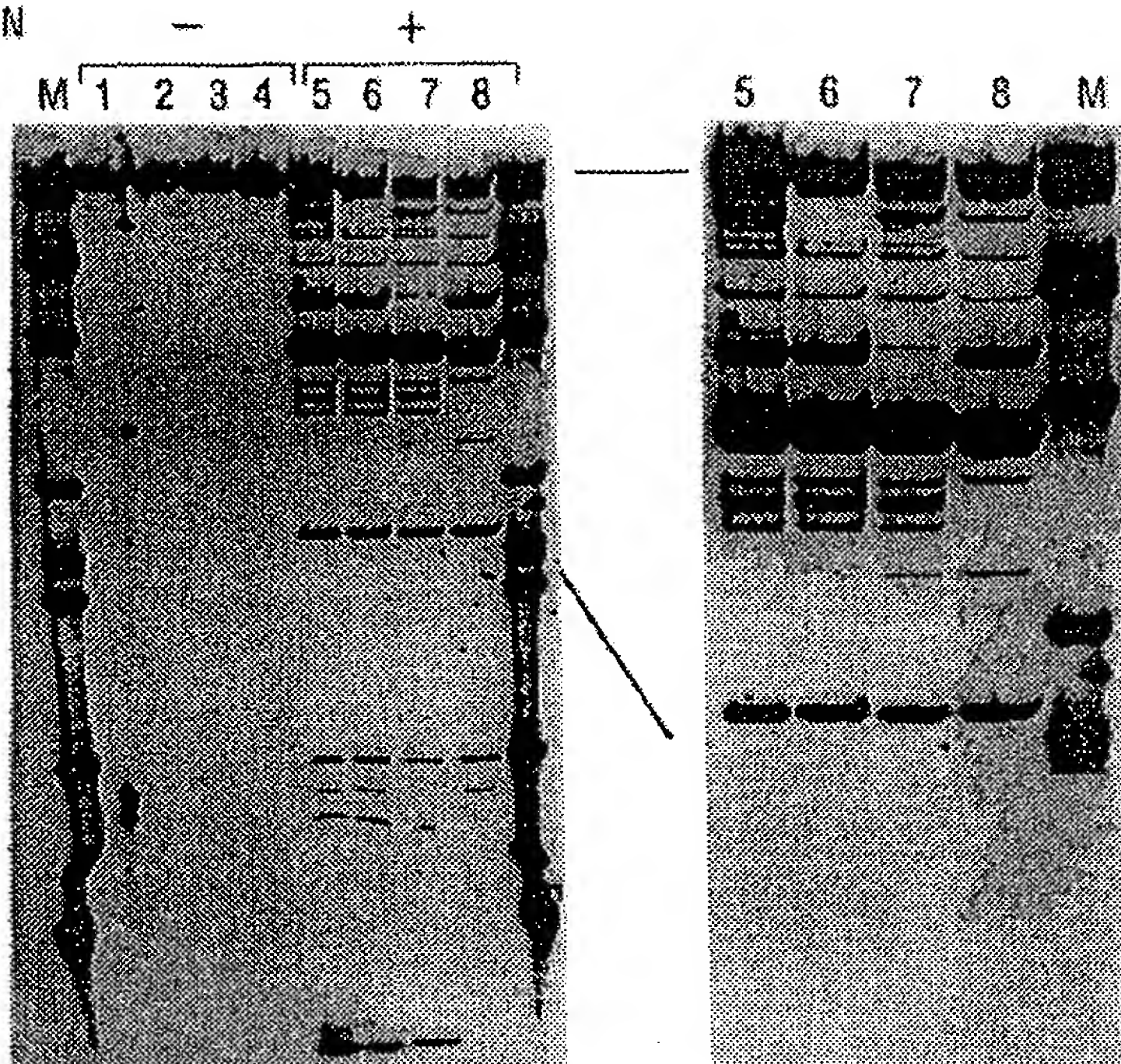


FIG. 43

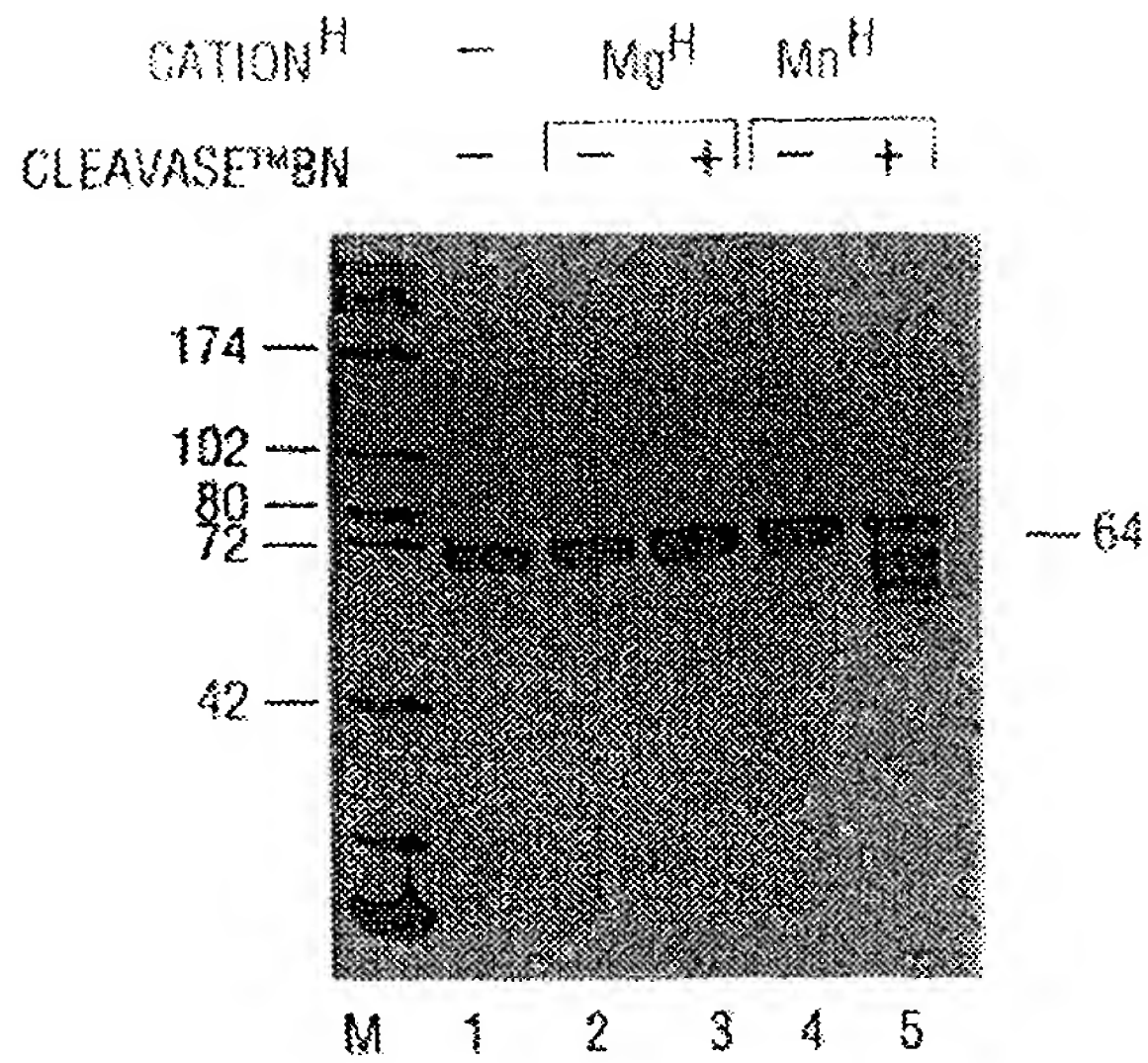


FIG. 44

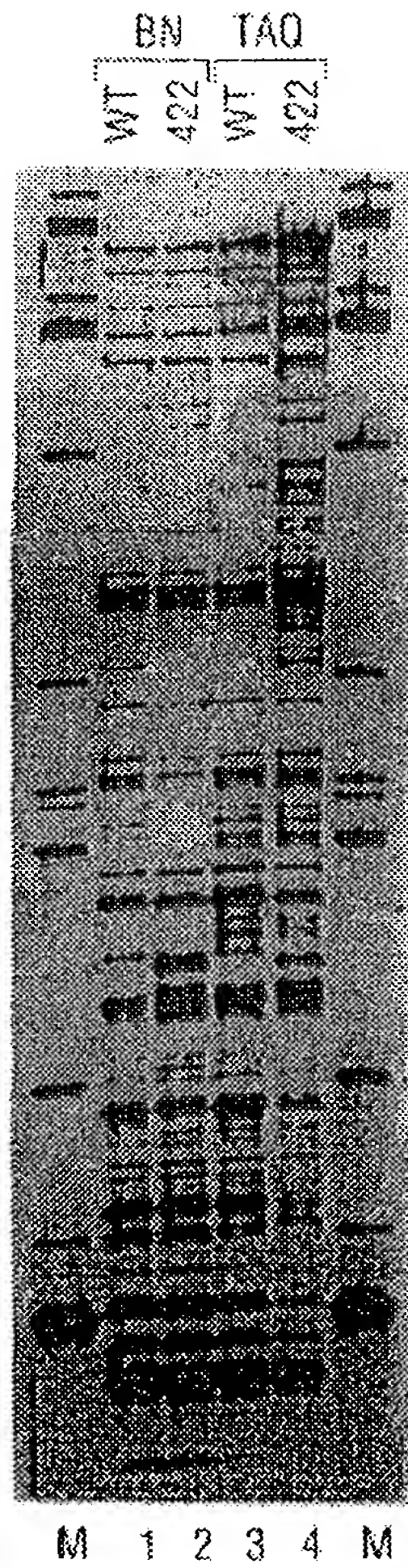


FIG. 45



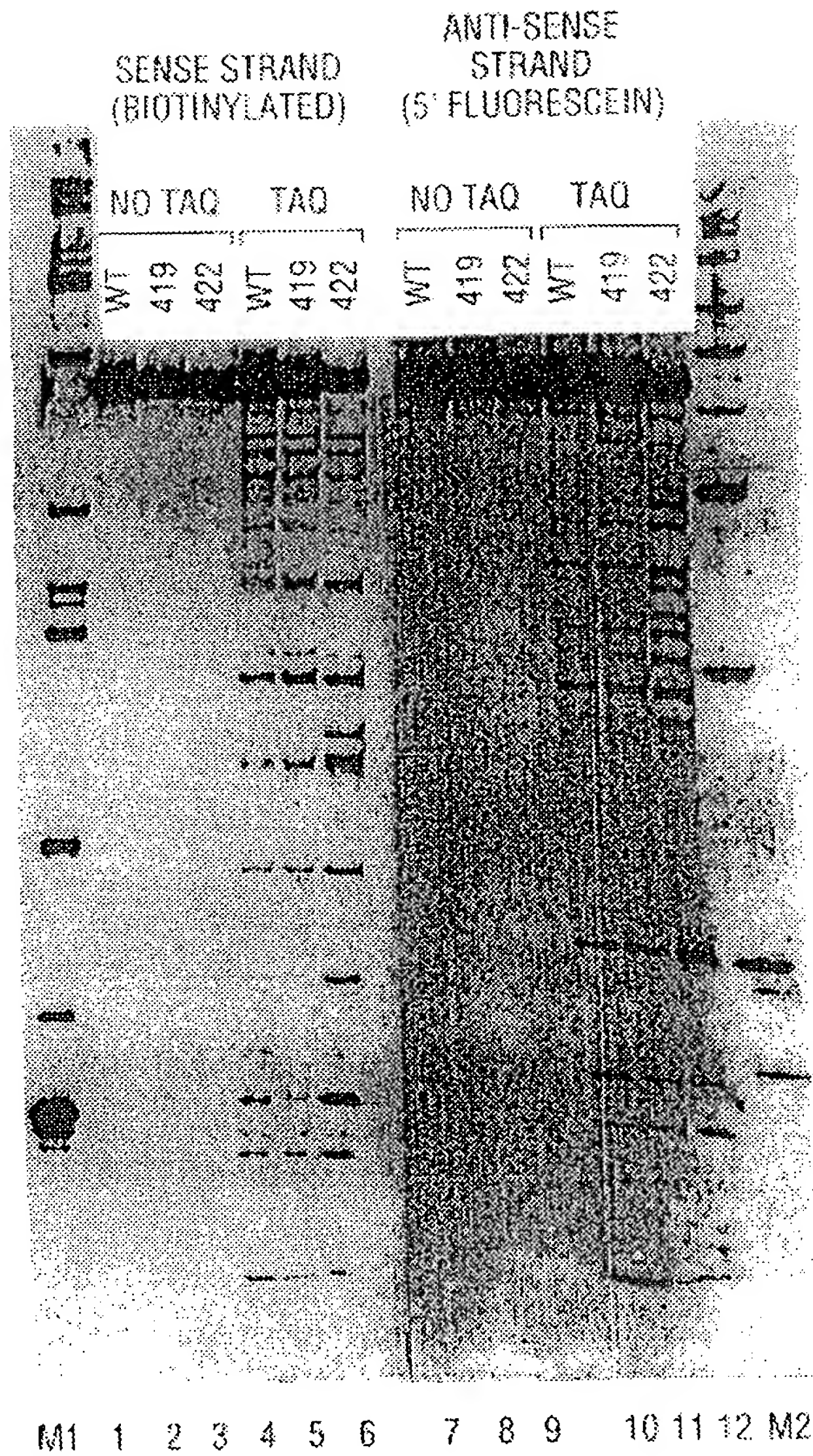


FIG. 46

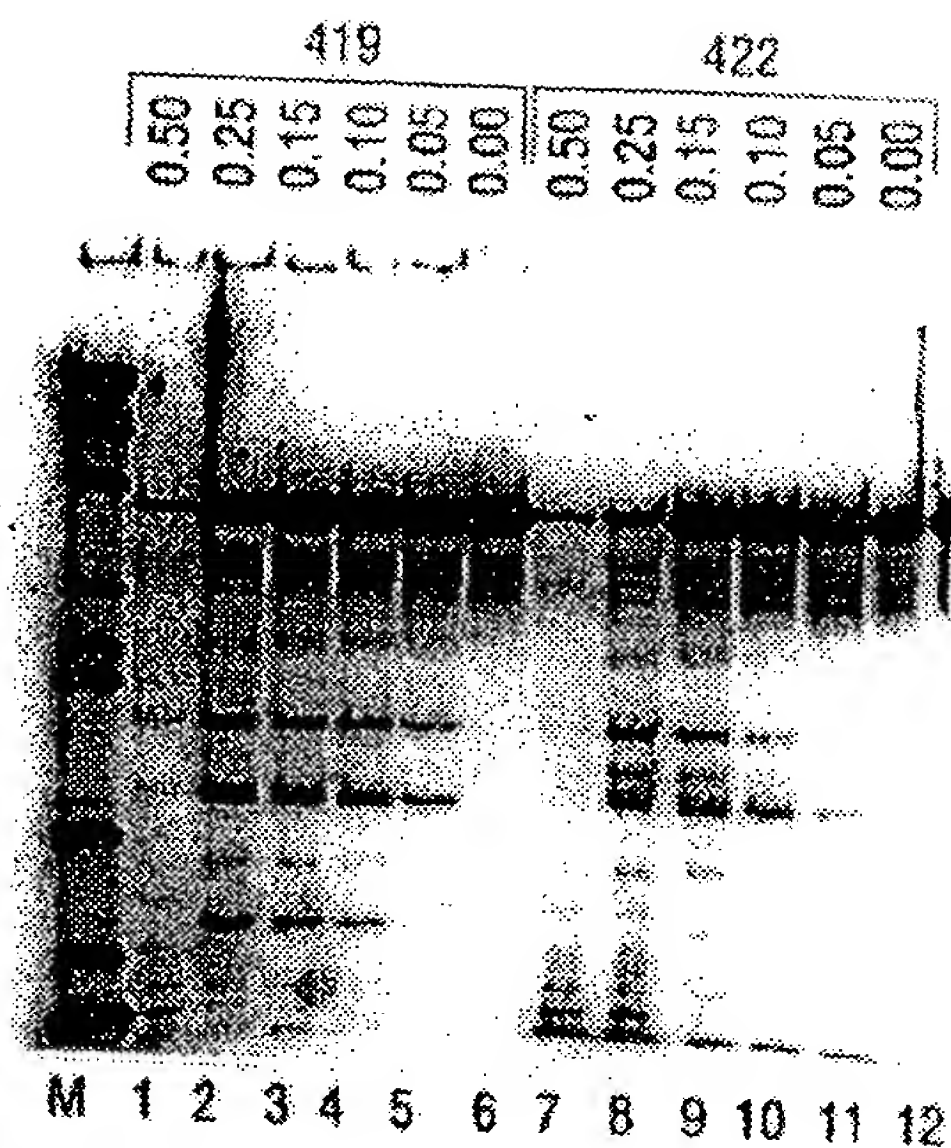


FIG. 47

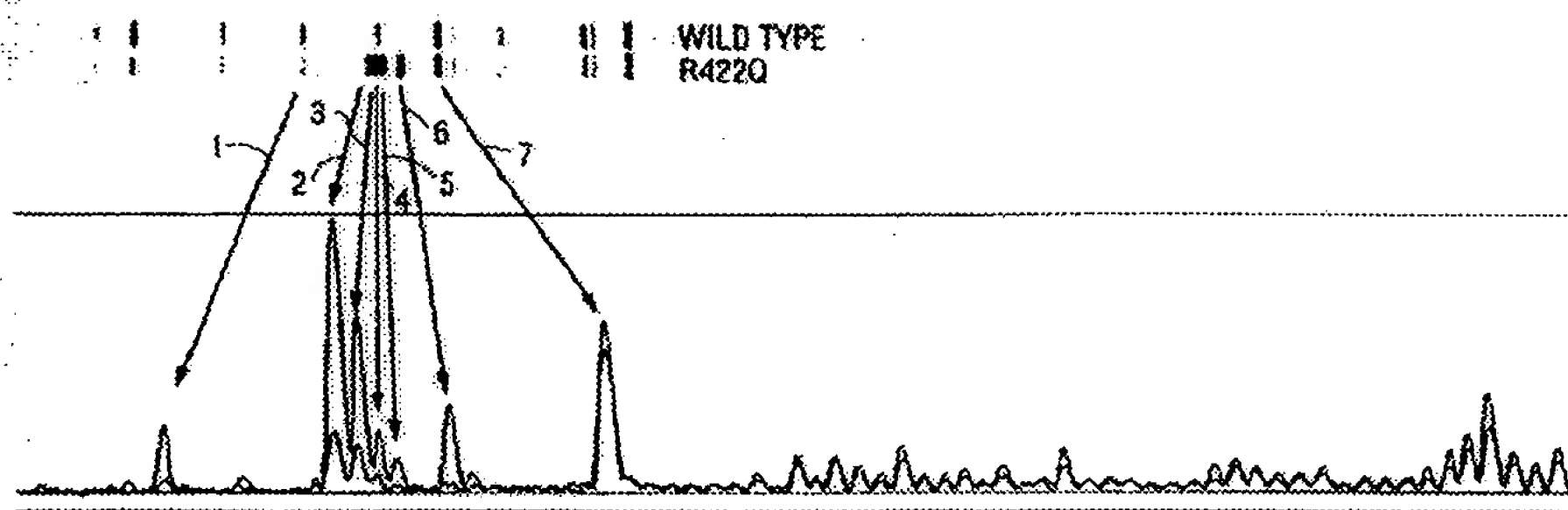


FIG. 48

50

L.100.8-1            5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
 (SEQ ID NO: 76) 3' CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCTGAAAGGTGTTCCCC

L.46.16-10           5' GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG  
 (SEQ ID NO: 77) 3' CCGACTGTTCTTCCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12           5' GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG  
 (SEQ ID NO: 78) 3' CCGACTGTTCTTCCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3            5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
 (SEQ ID NO: 79) 3' CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251            5' GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG  
 (SEQ ID NO: 80) 3' CCGACTGTTCTTCCCTTGAGCGACTTTGTGTCGTCCTGAAAGGTGTTCCCC

L.36.8-3            5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG  
 (SEQ ID NO: 81) 3' CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A



L.100.8-1		100
(SEQ ID NO: 76)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT	
	TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA	
L.46.16-10		
(SEQ ID NO: 77)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTTCT	
	TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGTGAAAGA	
L.46.16-12		
(SEQ ID NO: 78)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCACTTTTCT	
	TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGTGAAAGA	
L19.16-3		
(SEQ ID NO: 19)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCTCTCTCT	
	TACAATGCCCTCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA	
L.CEM/251		
(SEQ ID NO: 80)	ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTTCT	
	TACAATGCCCCCTCCATGACCCCTTCCTCGGCCAGCCCTTGCGGGTGAAAGA	
L.36.8-3		
(SEQ ID NO: 81)	ATGTTACGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCTCT	
	TACAATGCCCTCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA	

FIG. 49B

150

L. 100.8-1	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCCGGA 3'ACCACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L. CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT

**FIG. 49C**

L. 100. 8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	200
L. 46. 16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L. 46. 16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L. 19. 16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L. CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC	
L. 36. 8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D

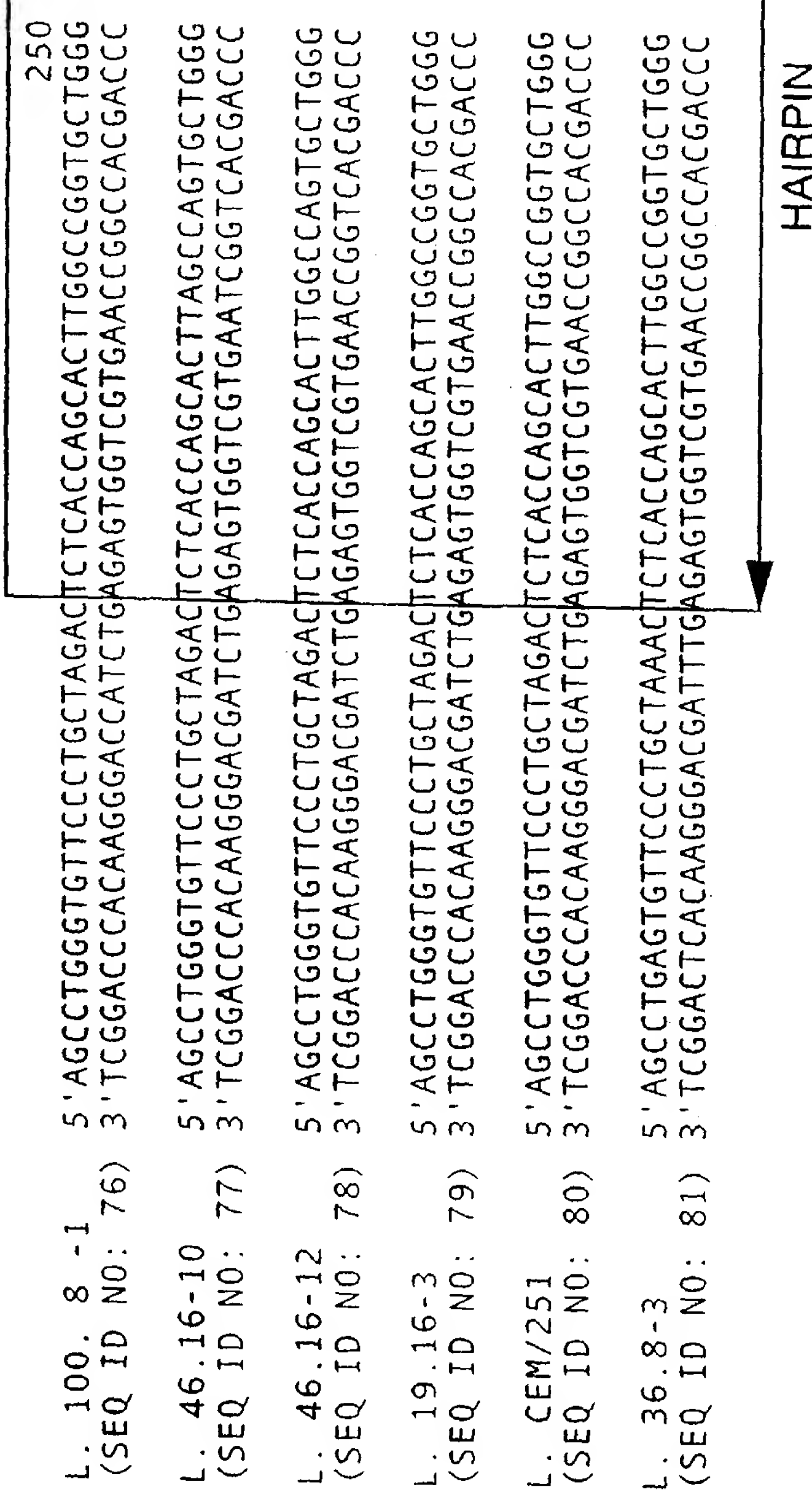


FIG. 49E

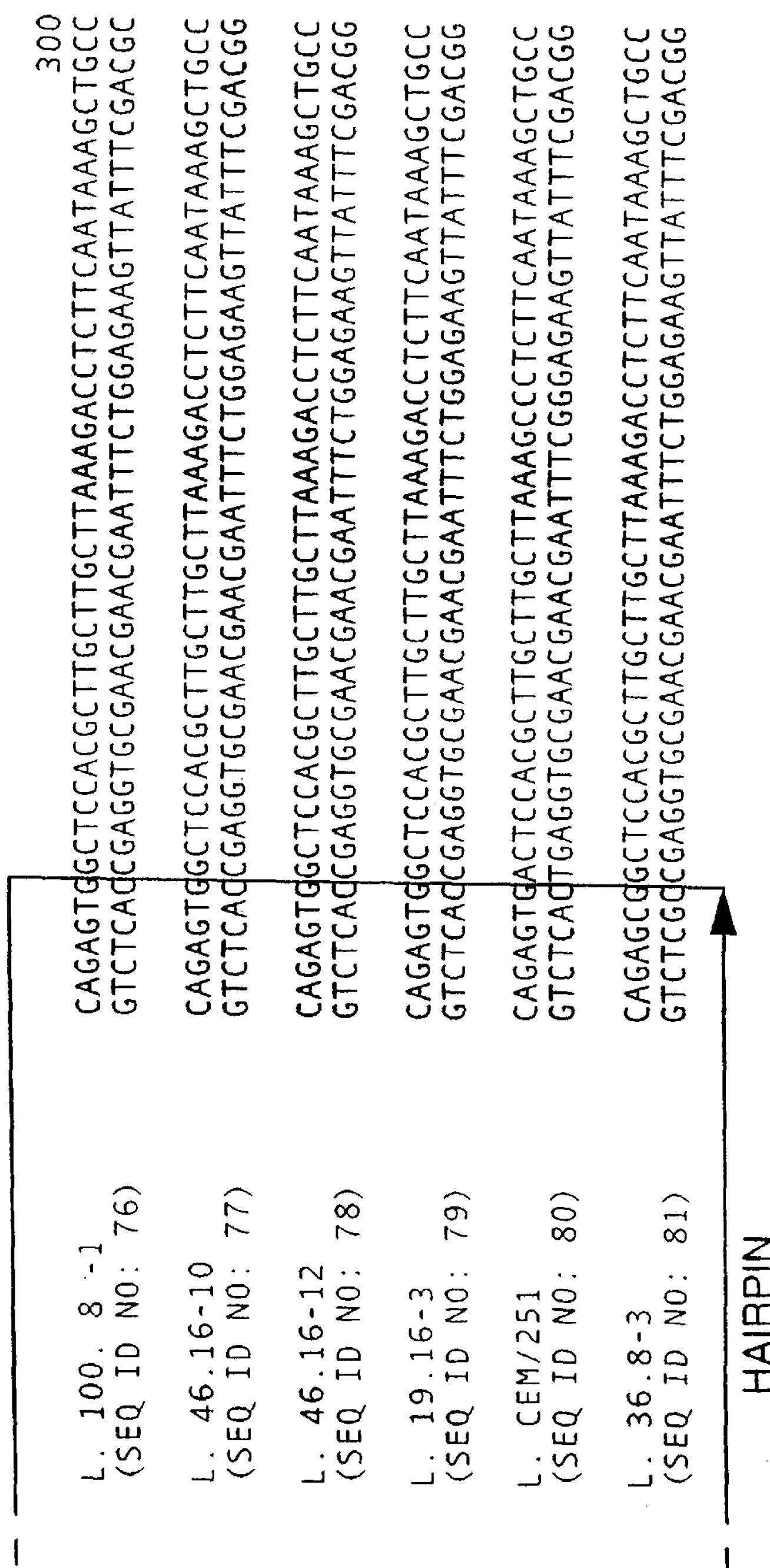


FIG. 49F

L.100.8-1	5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG	350	G 3'
	3'TAAATCTTTCATCCGGTCACACACAAGGGTAGAGAGGATCGGCGGGGAC		C 5'
L.46,16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG		G 3'
	3'TAAATCTTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCGGGGAC		C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG		G 3'
	3'TAAATCTTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCGGGGAC		C 5'
L.19,16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG		G 3'
	3'TAAATCTTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGGGAC		C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG		G 3'
	3'TAAATCTTTCATTCGATCACACACAAGGGTAGAGAGGATCGGCGGGGAC		C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG		G 3'
	3'TAAATCTTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGGGAC		C 5'

FIG. 49G



FIG. 50

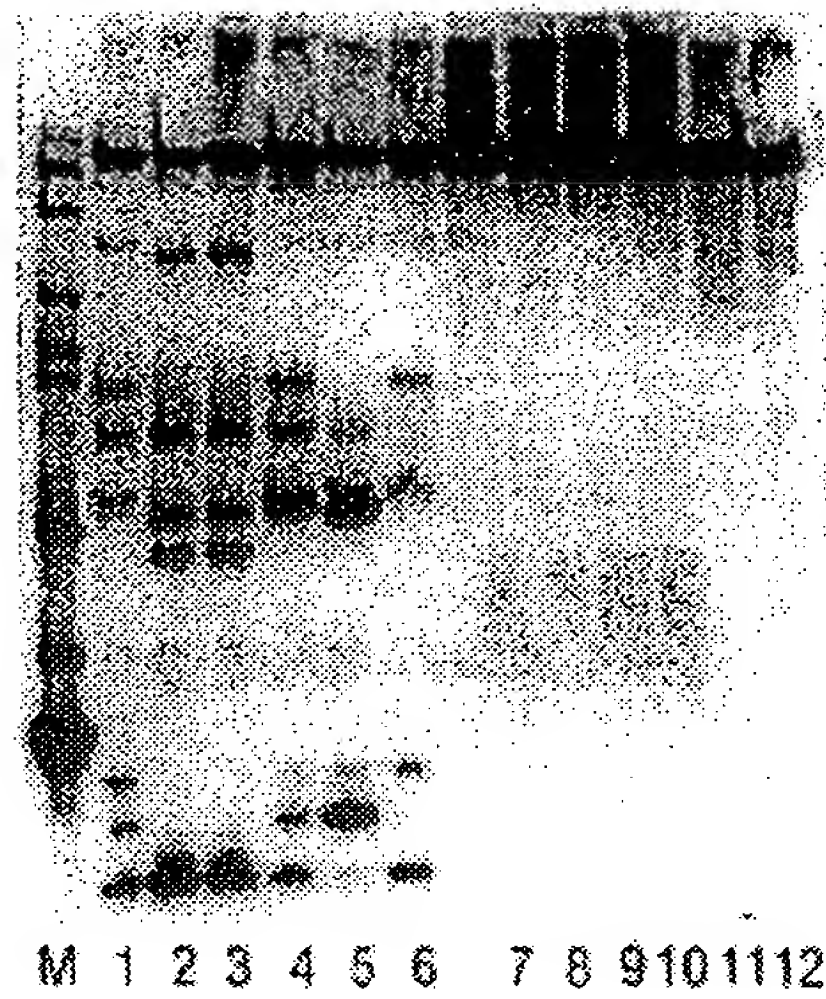


FIG. 51



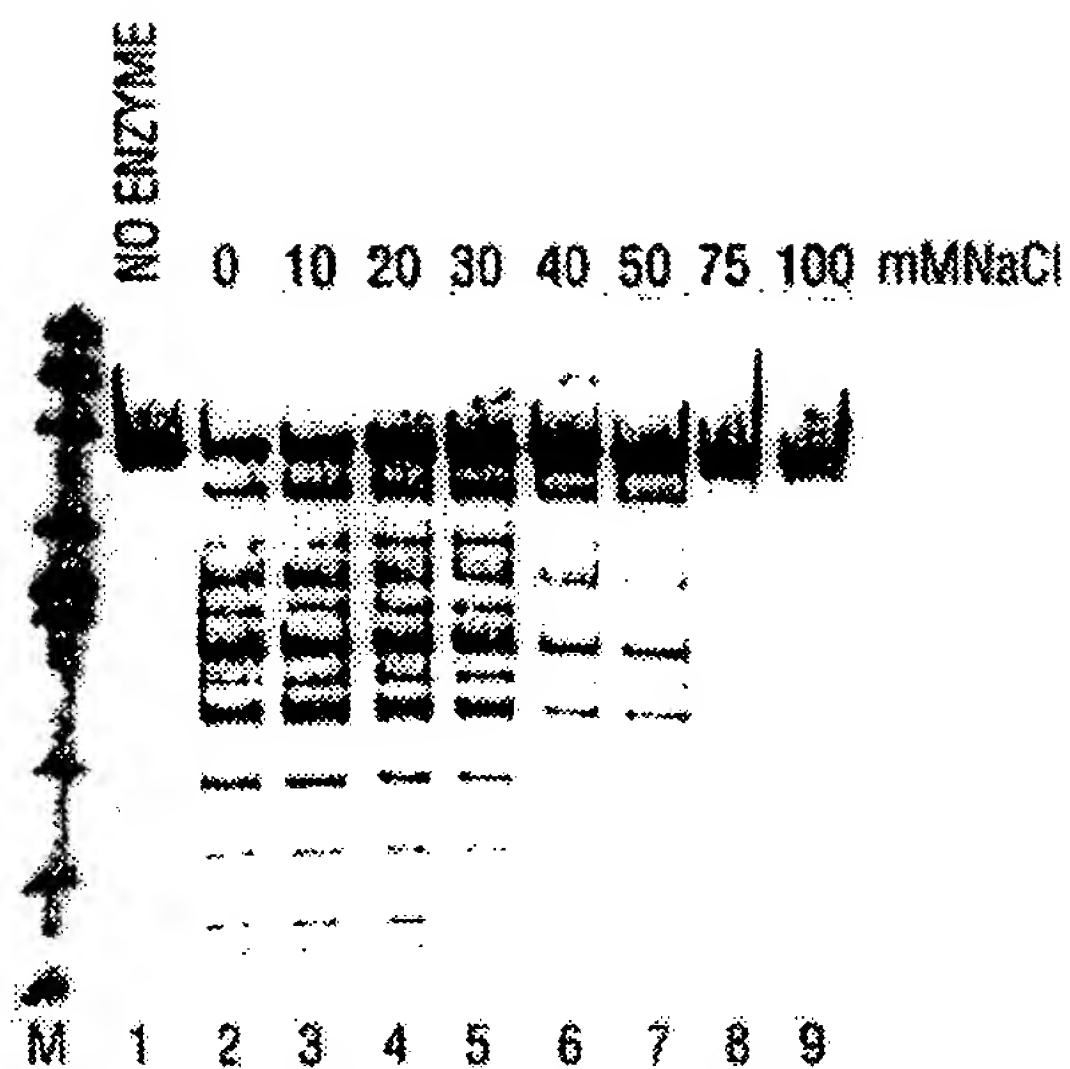


FIG. 52

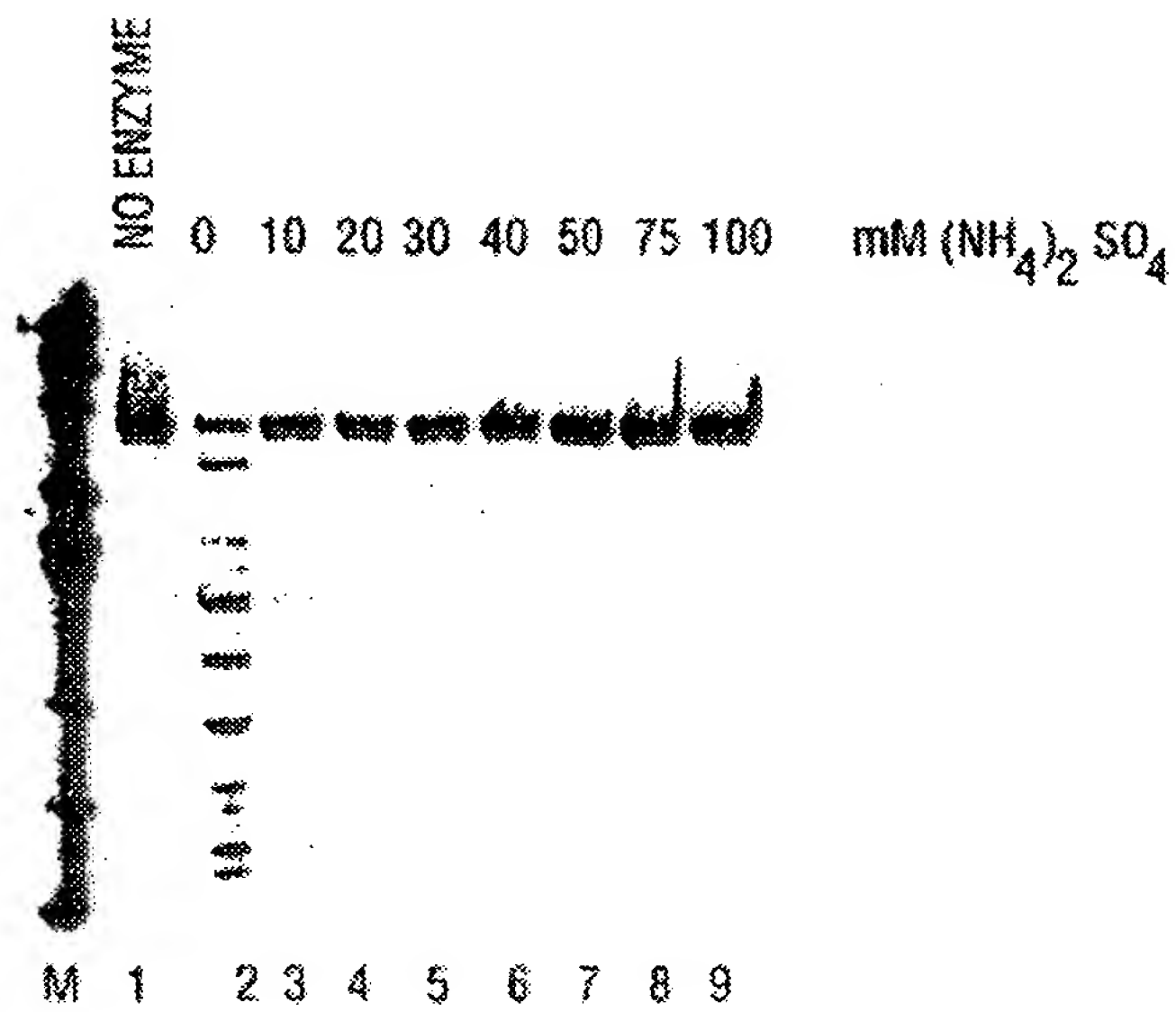


FIG. 53

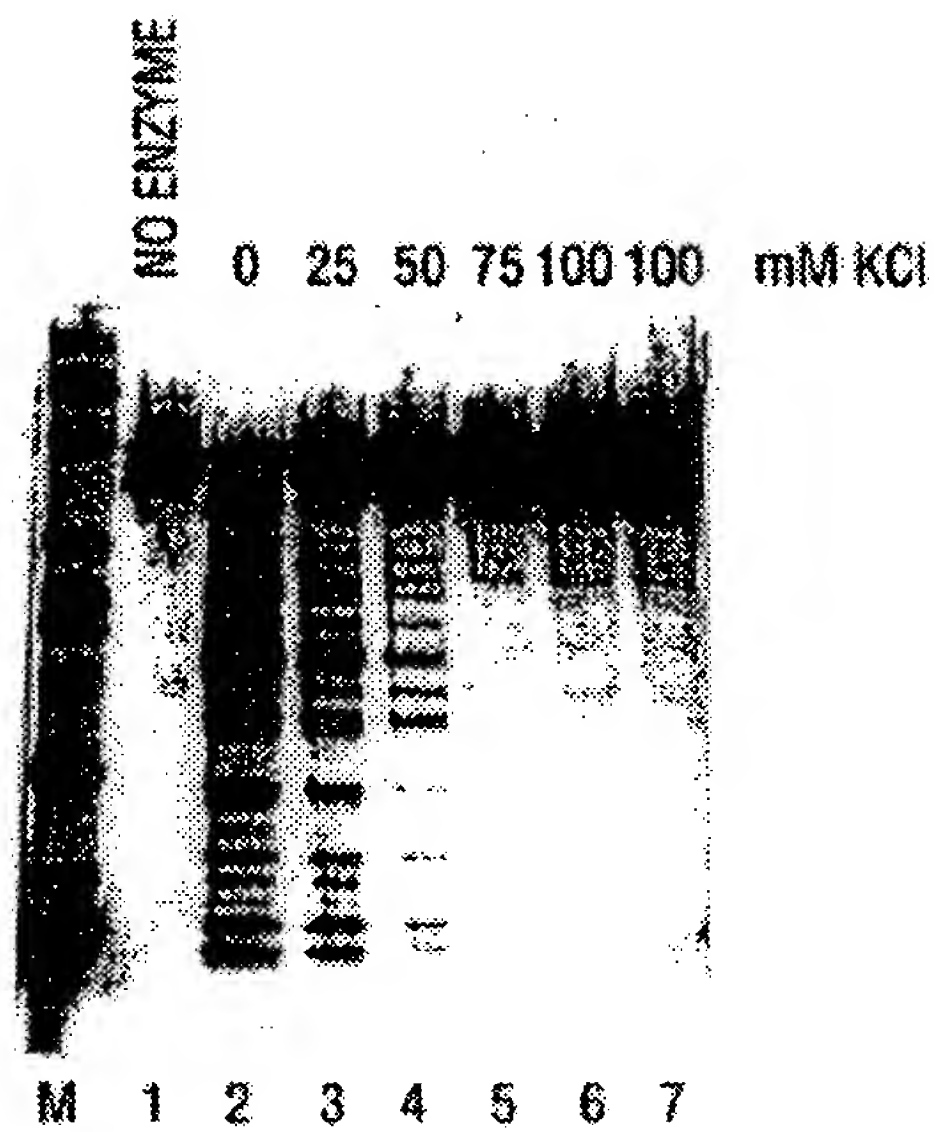


FIG. 54

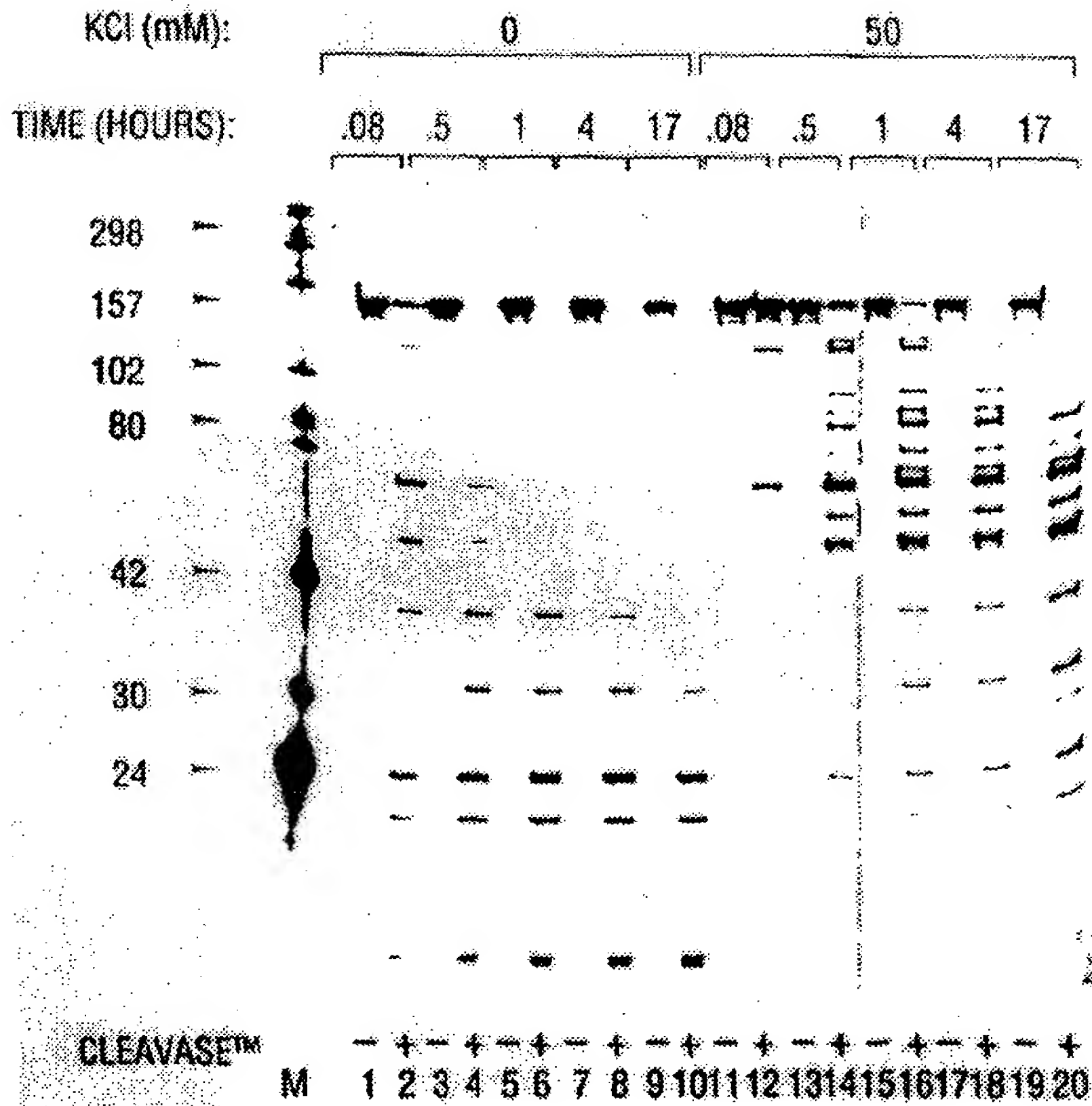


FIG. 55

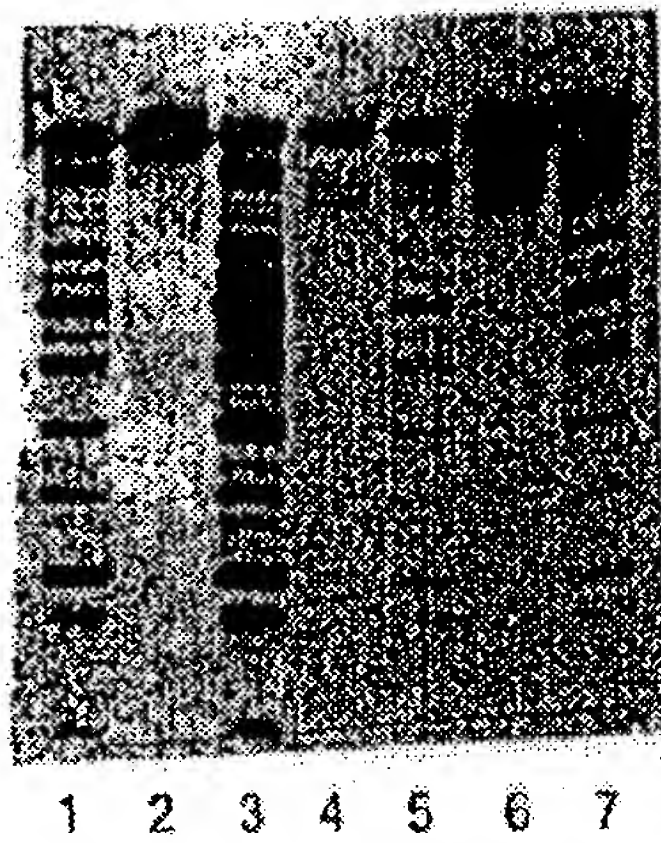


FIG. 56

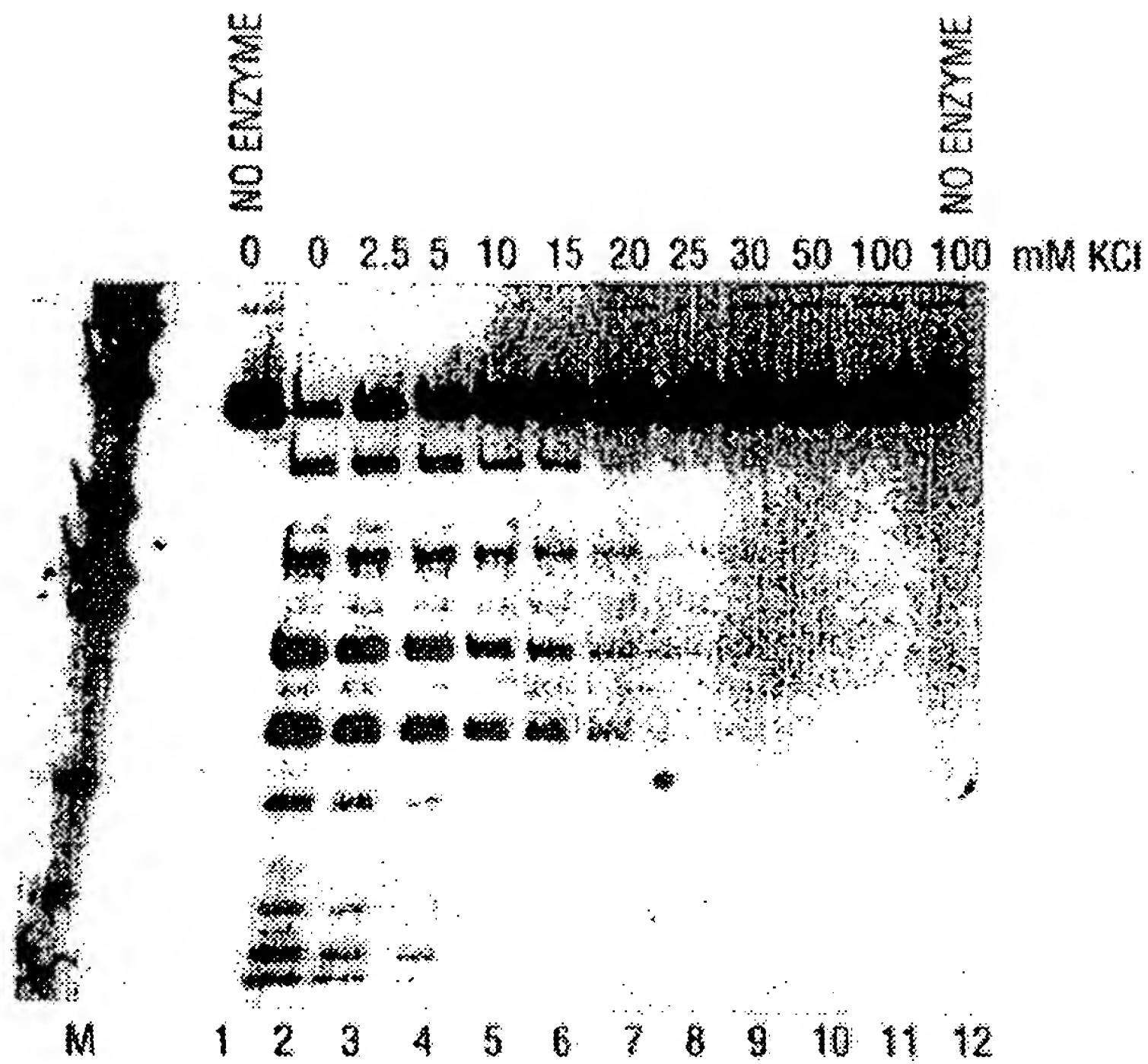


FIG. 57

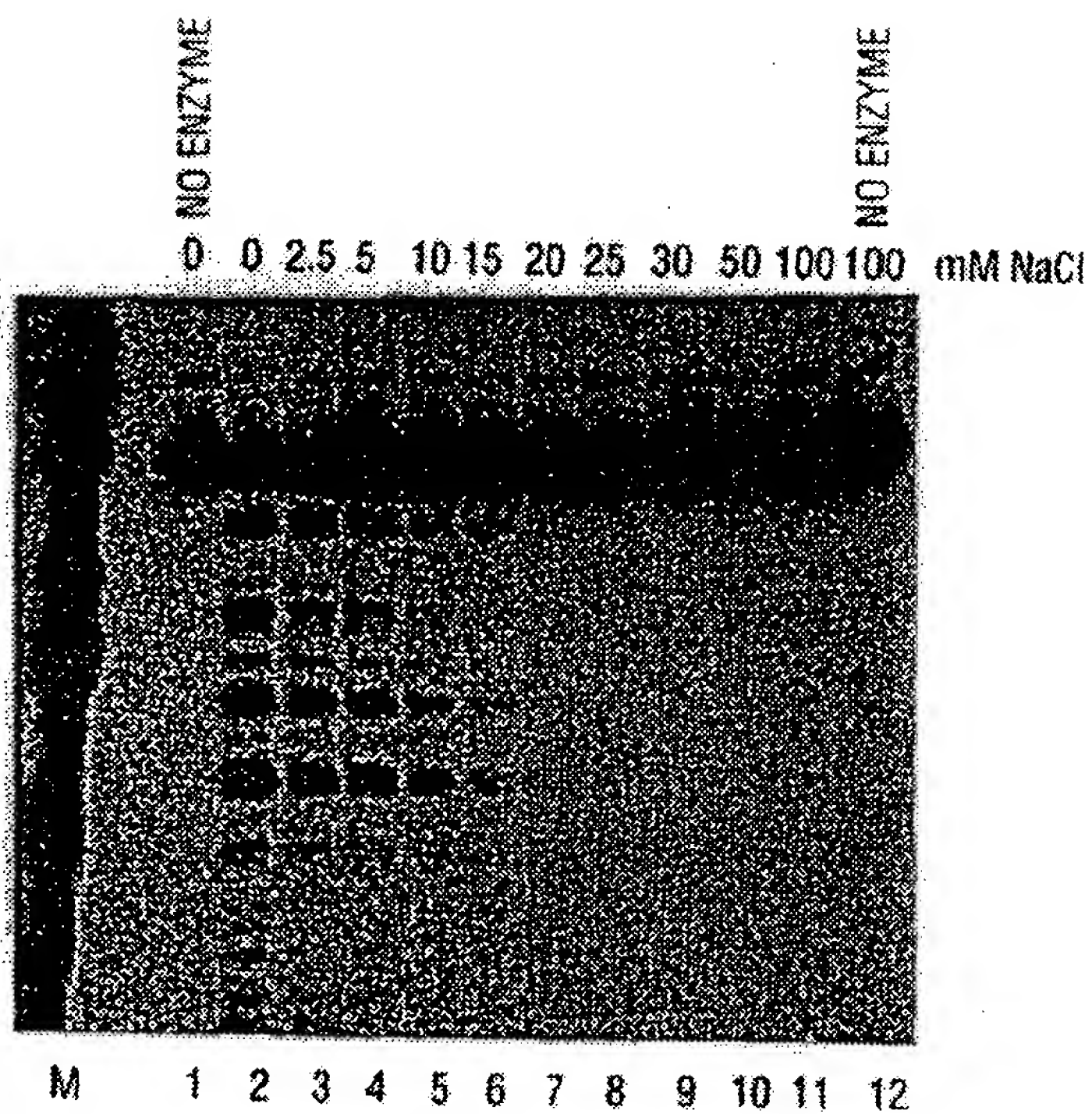


FIG. 58

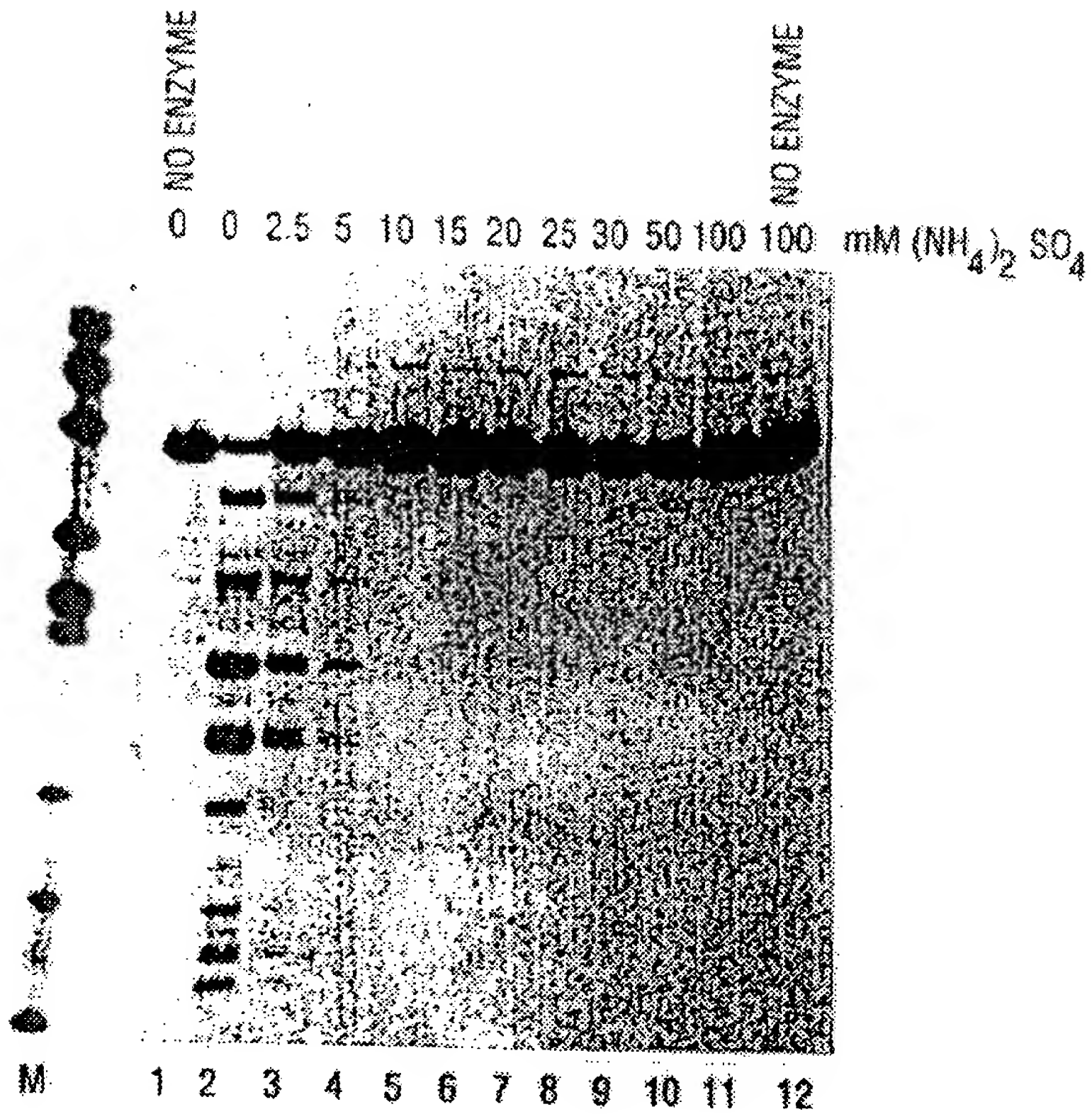


FIG. 59



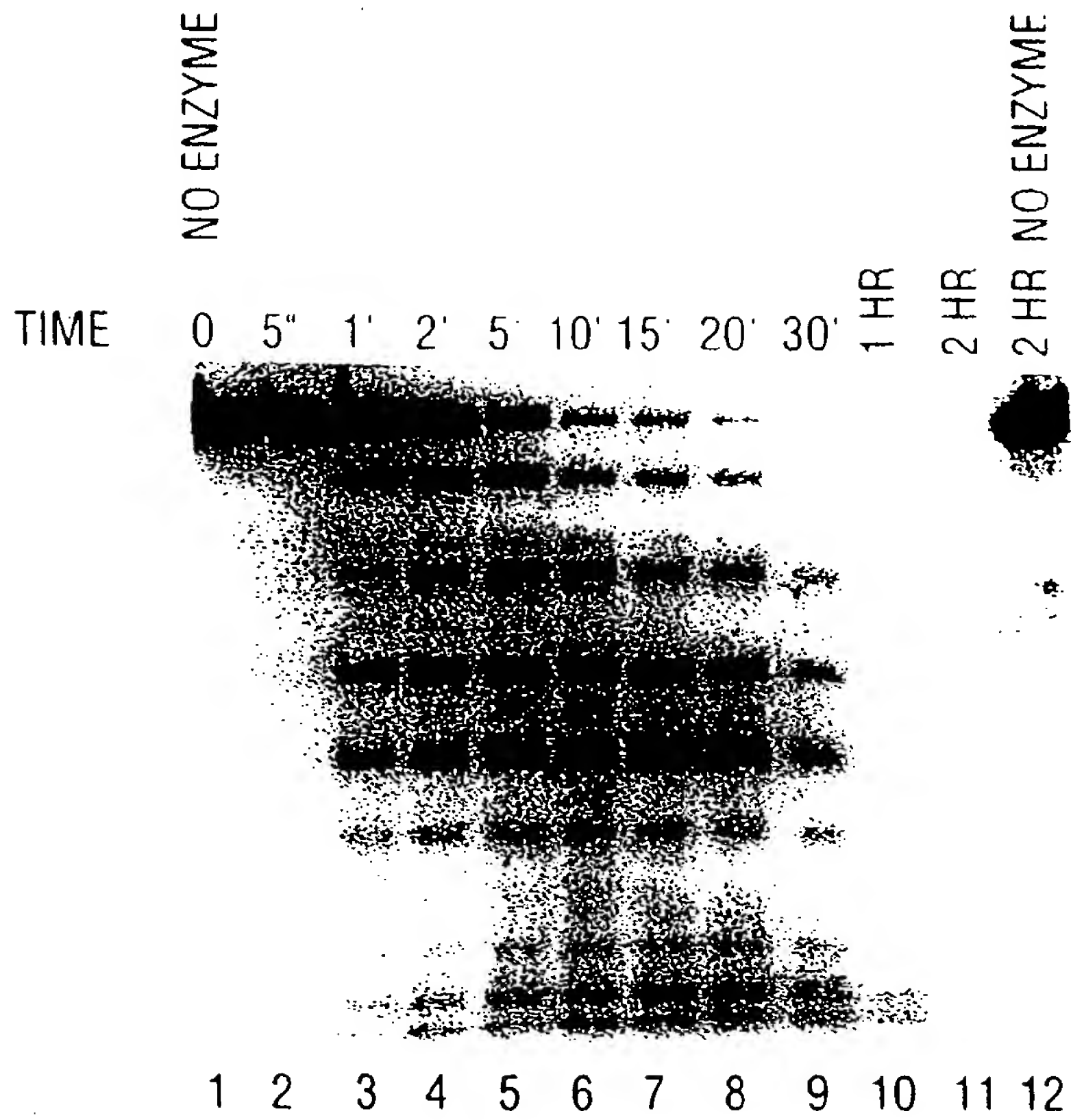


FIG. 60

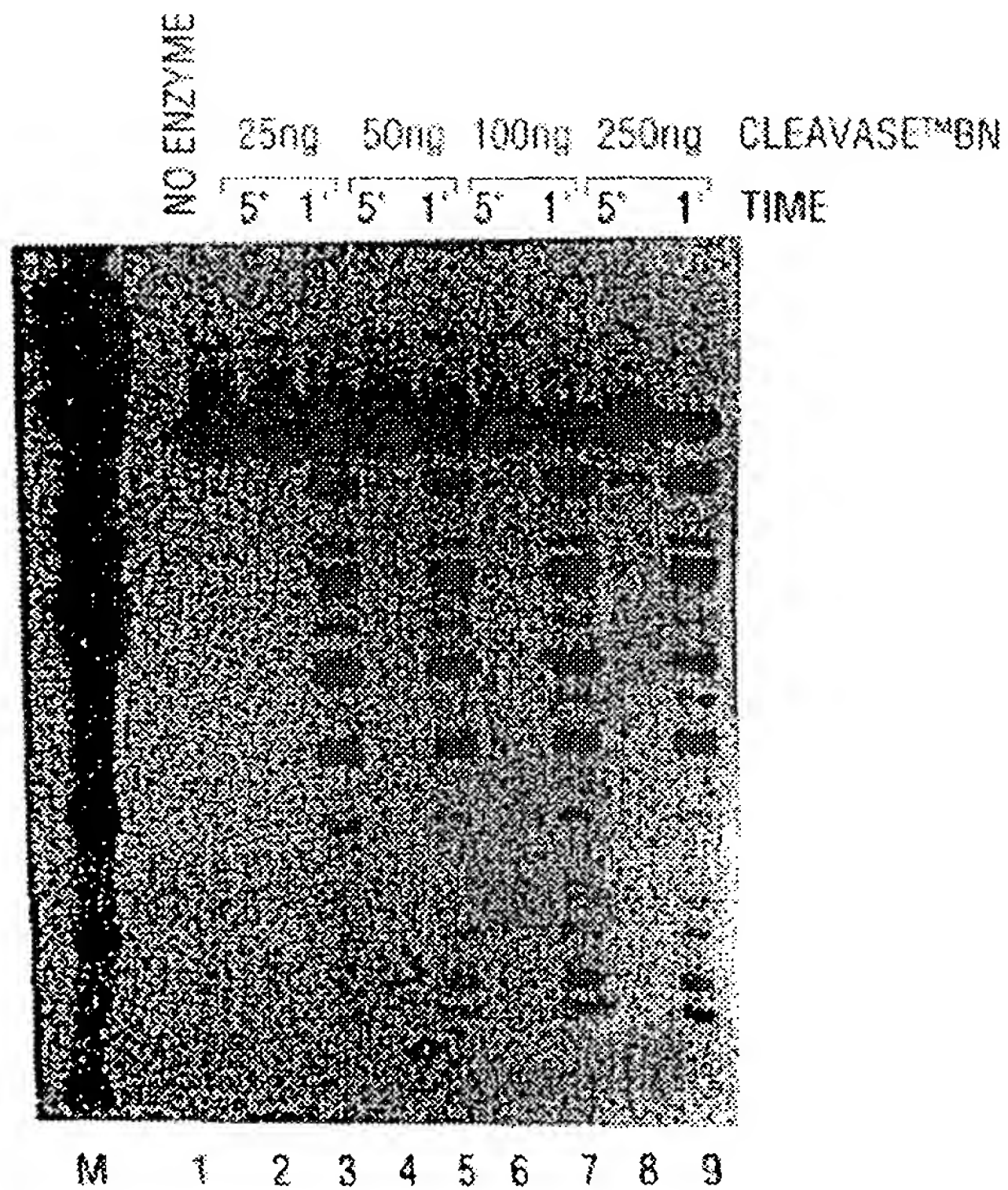


FIG. 61

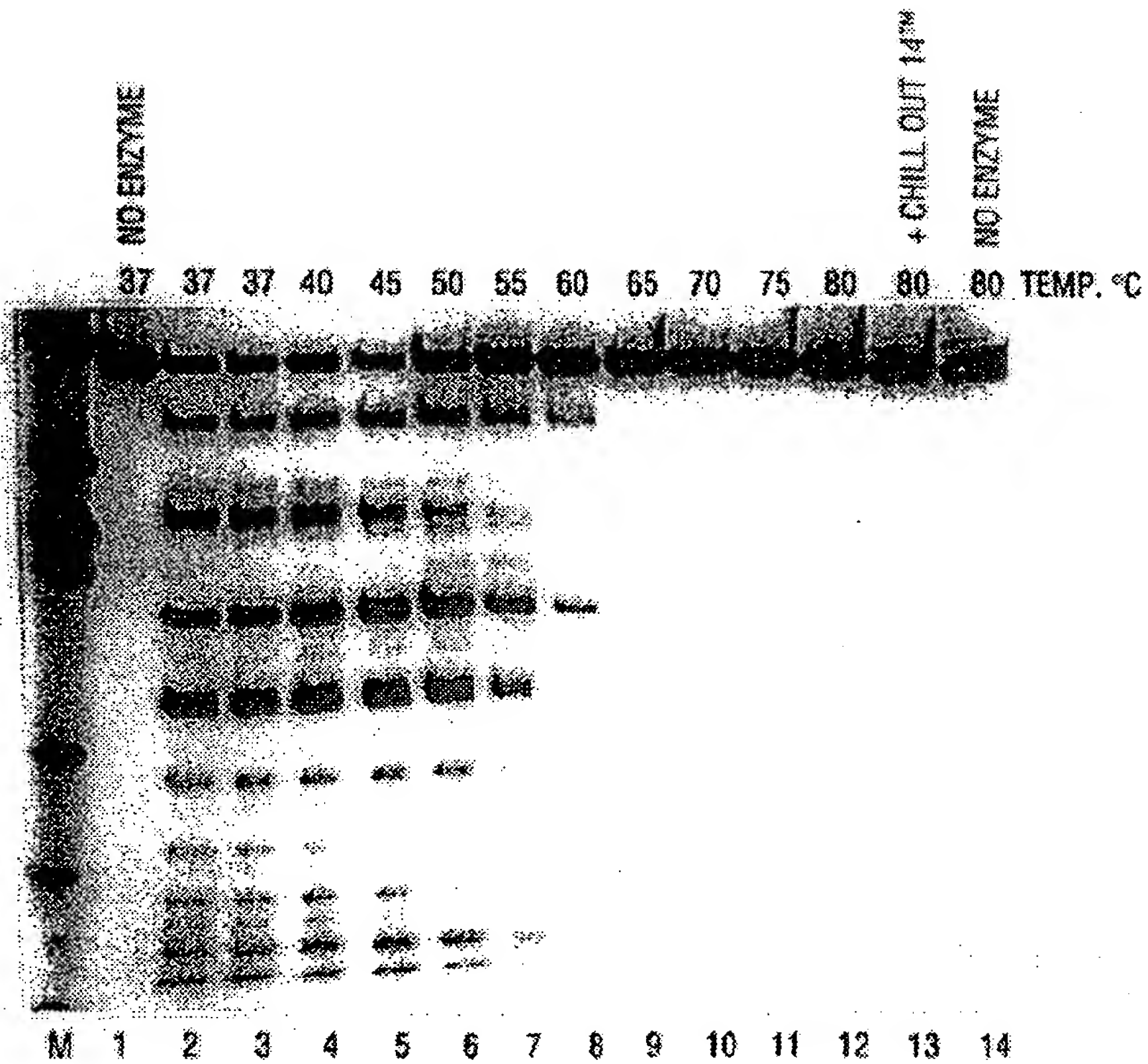


FIG. 62

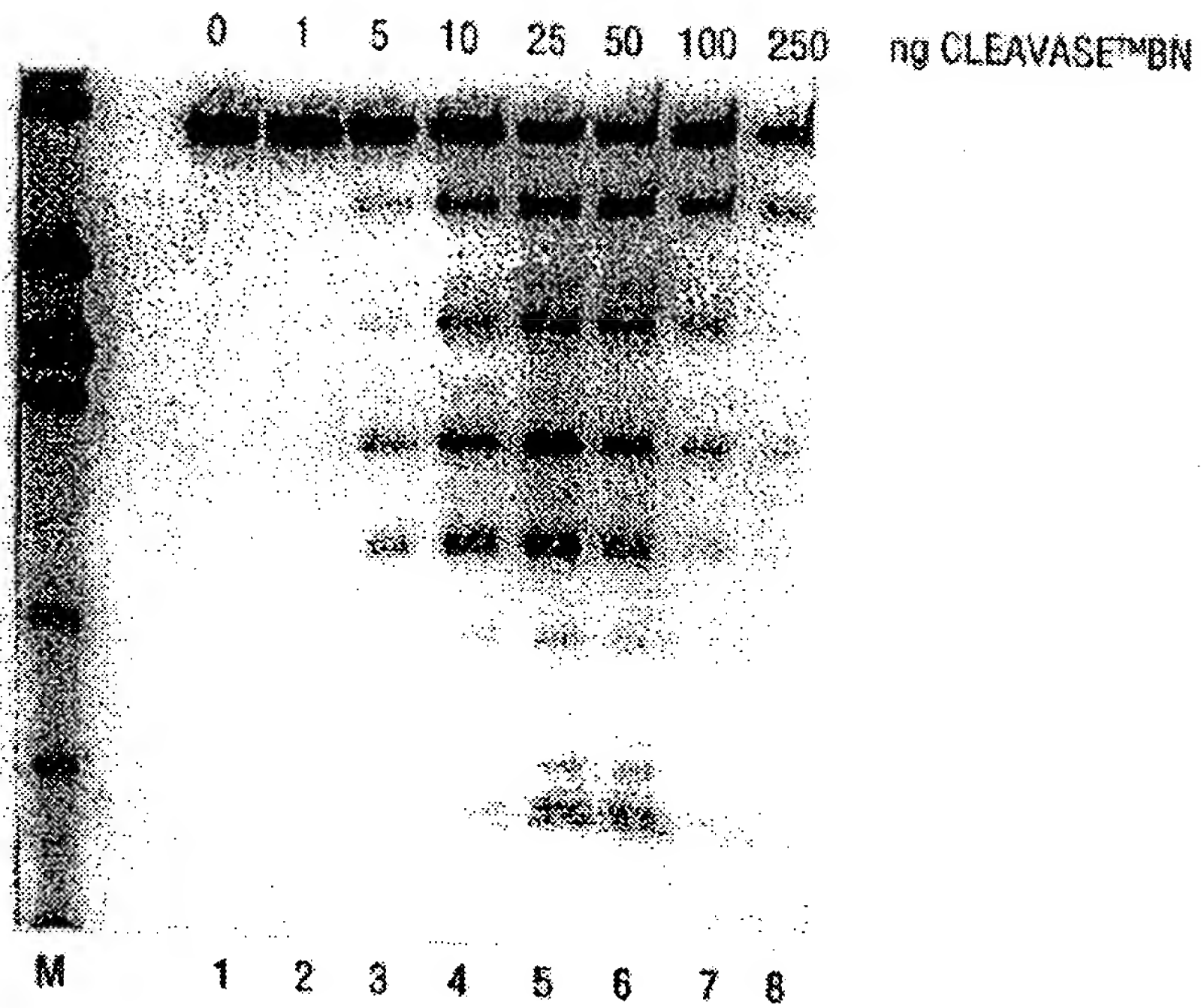


FIG. 63

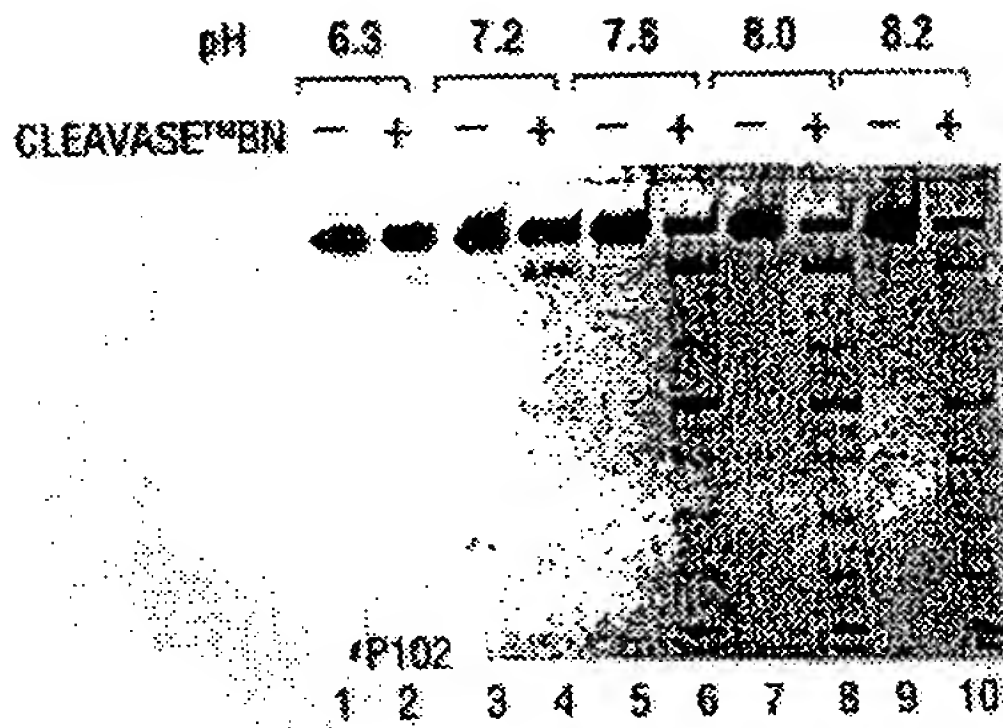


FIG. 64A

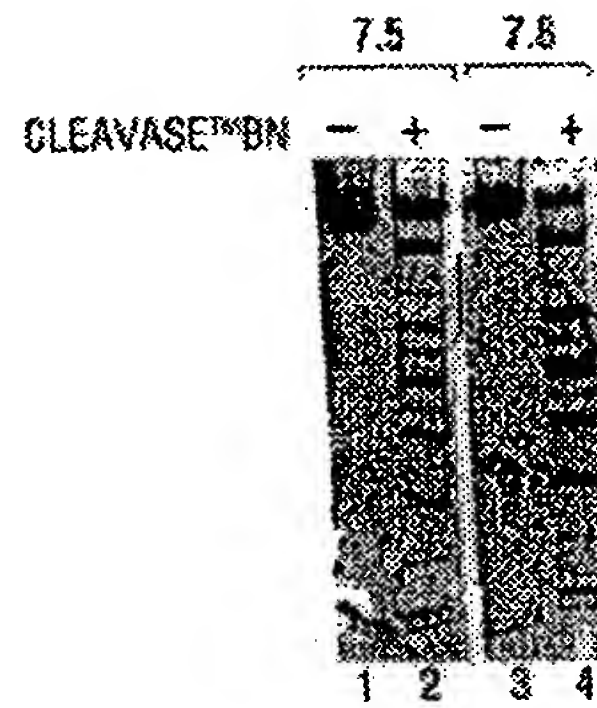


FIG. 64B

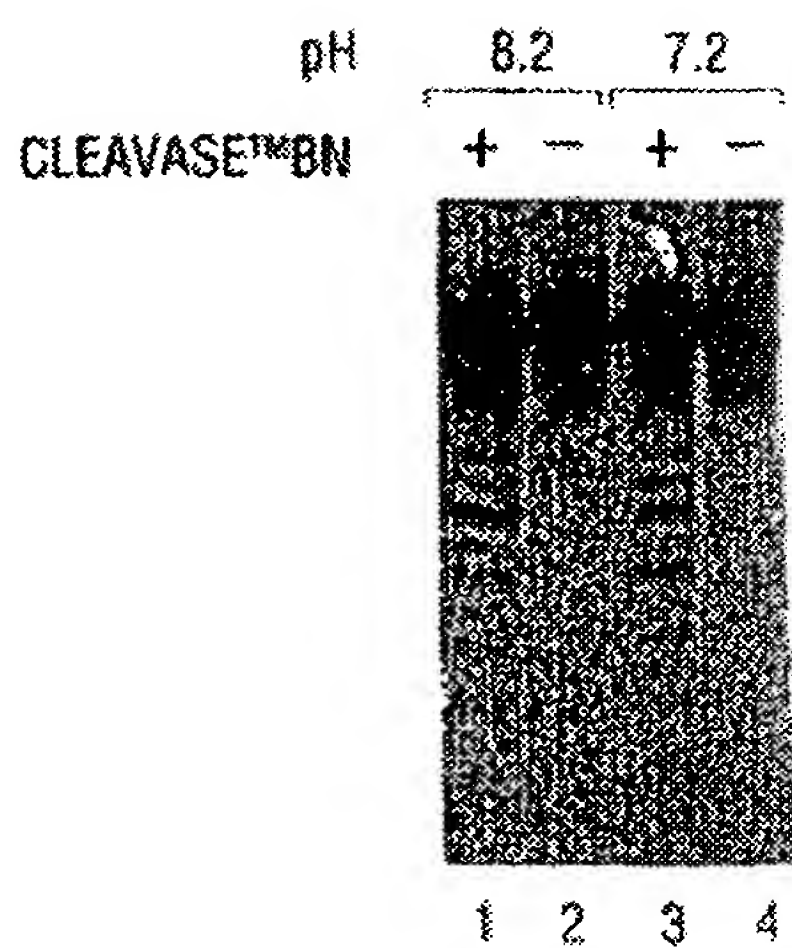


FIG. 65A

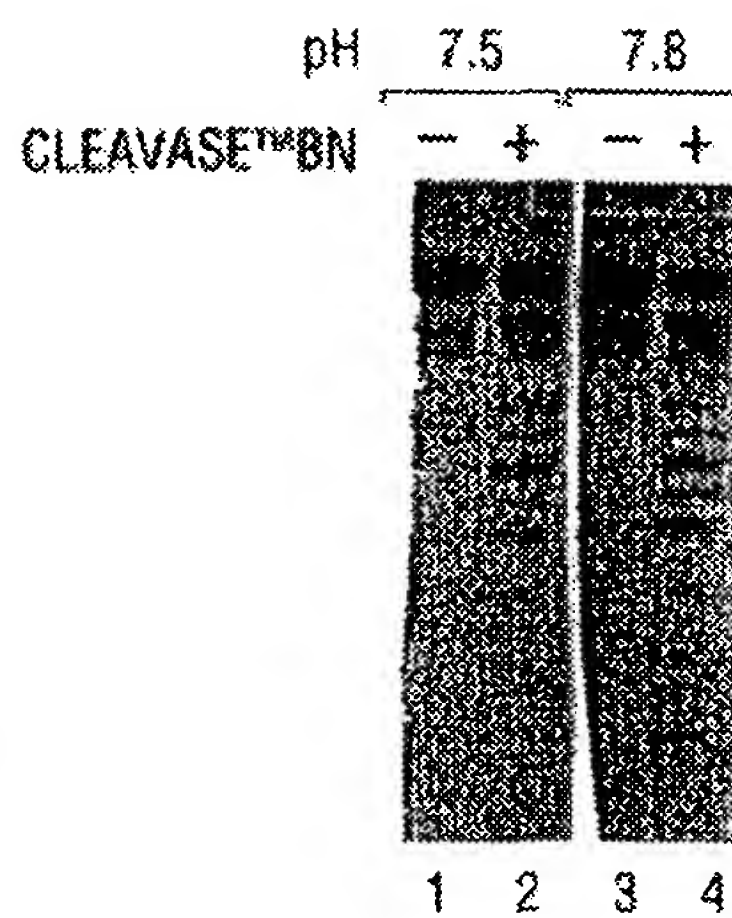


FIG. 65B

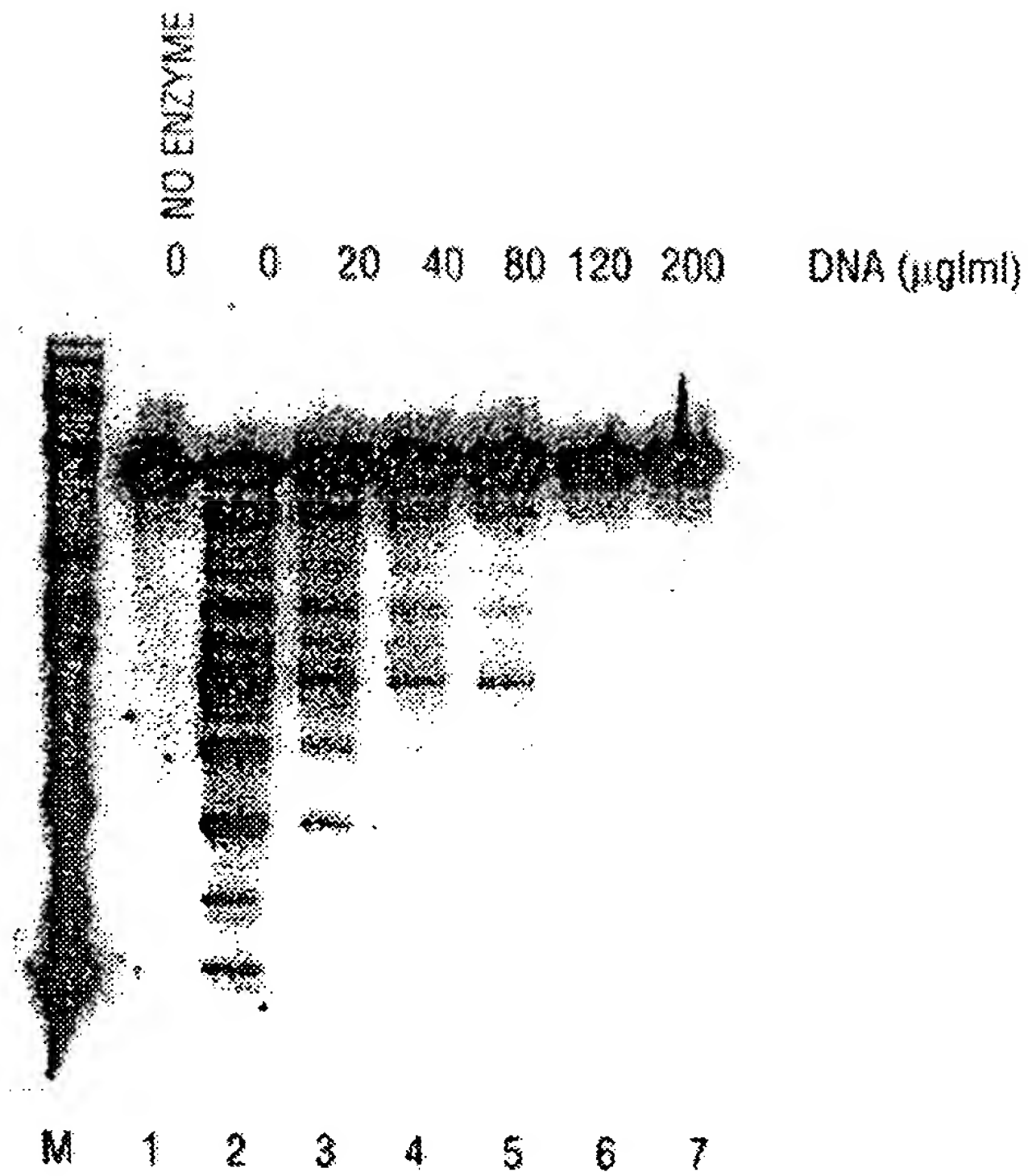


FIG. 66

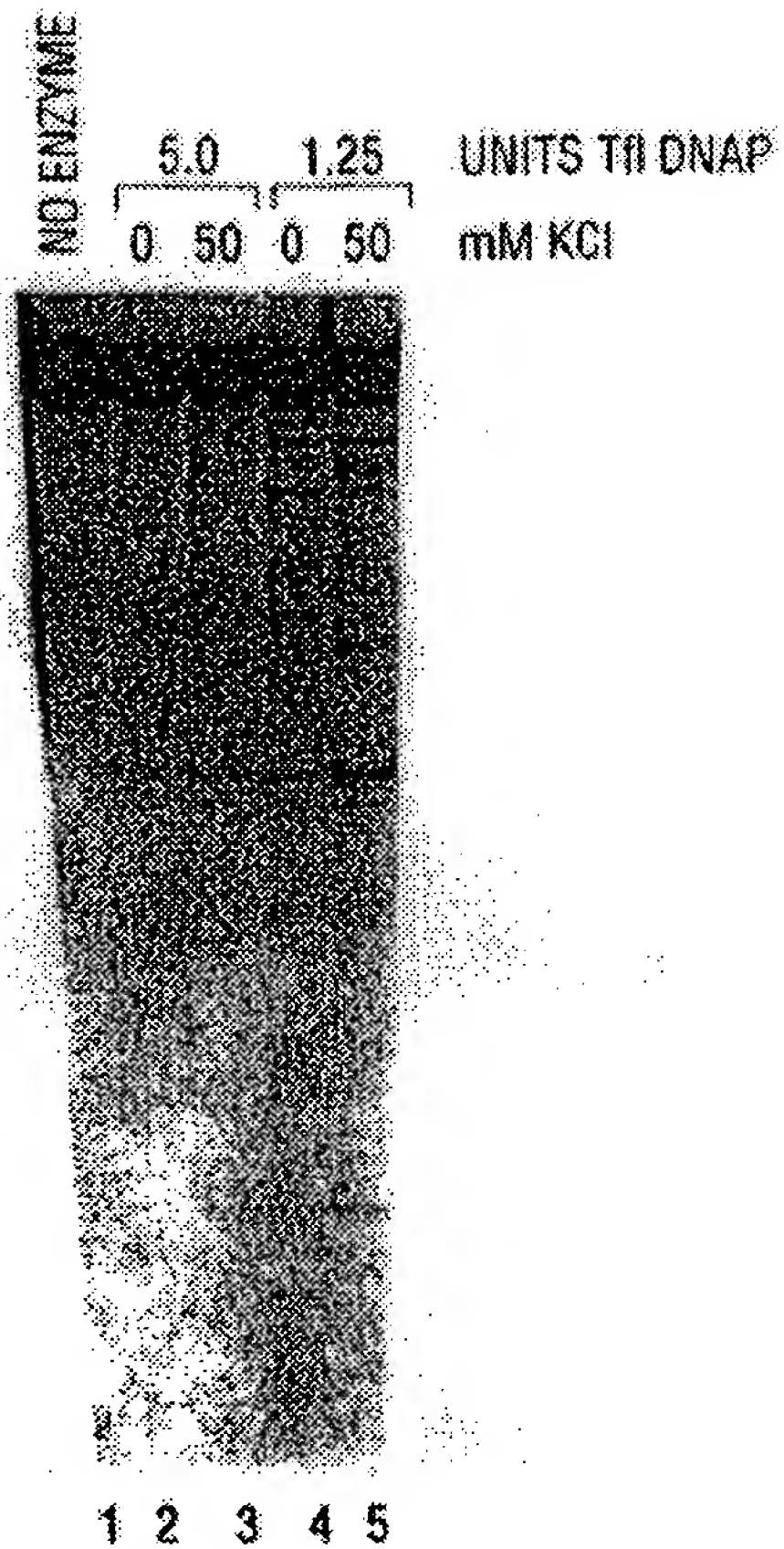


FIG. 67



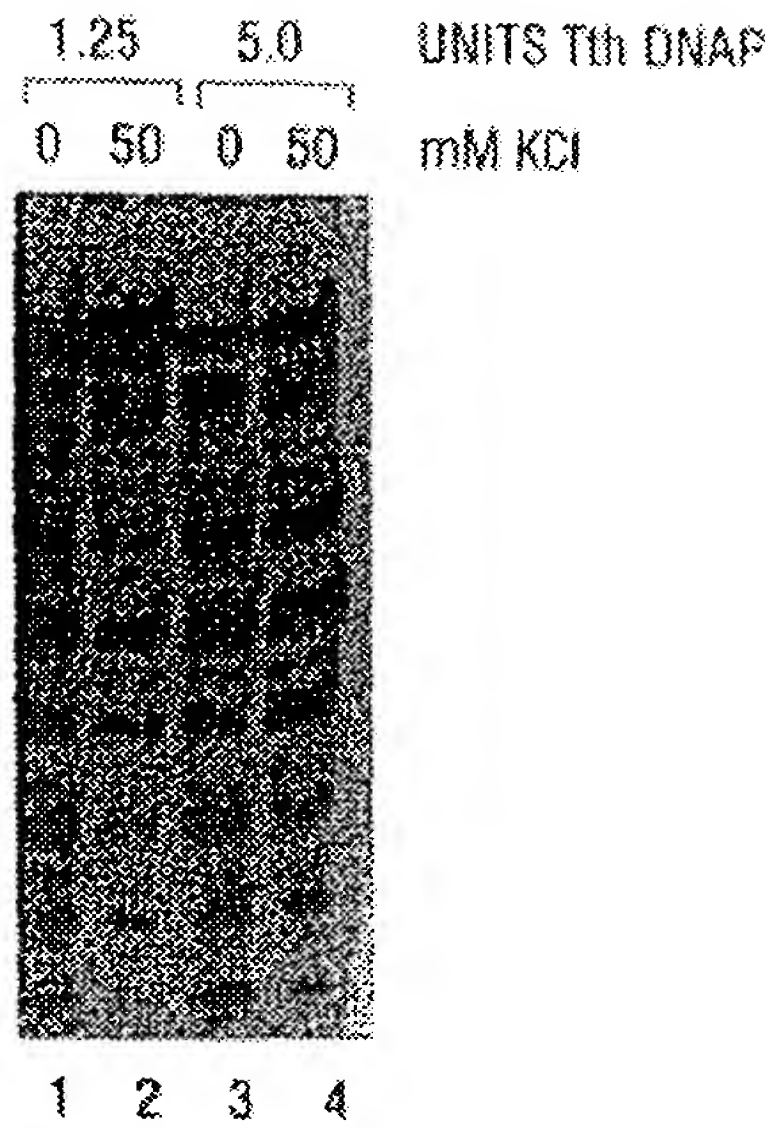


FIG. 68

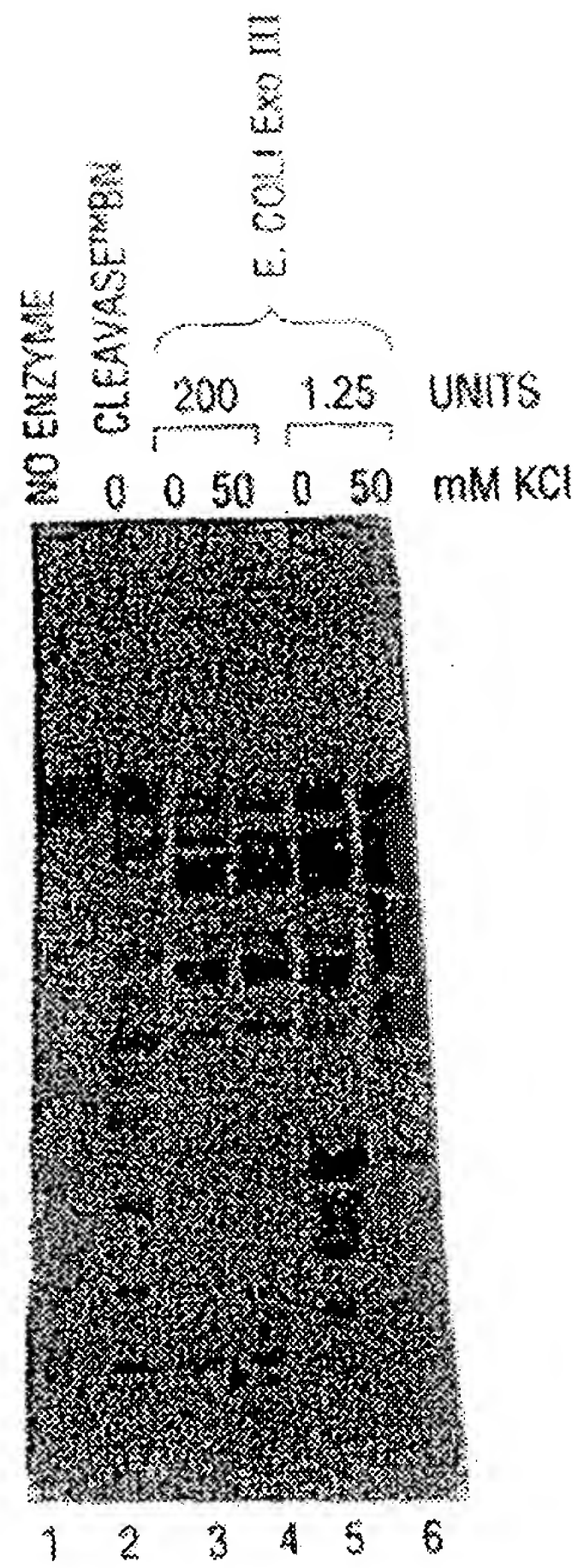


FIG. 69

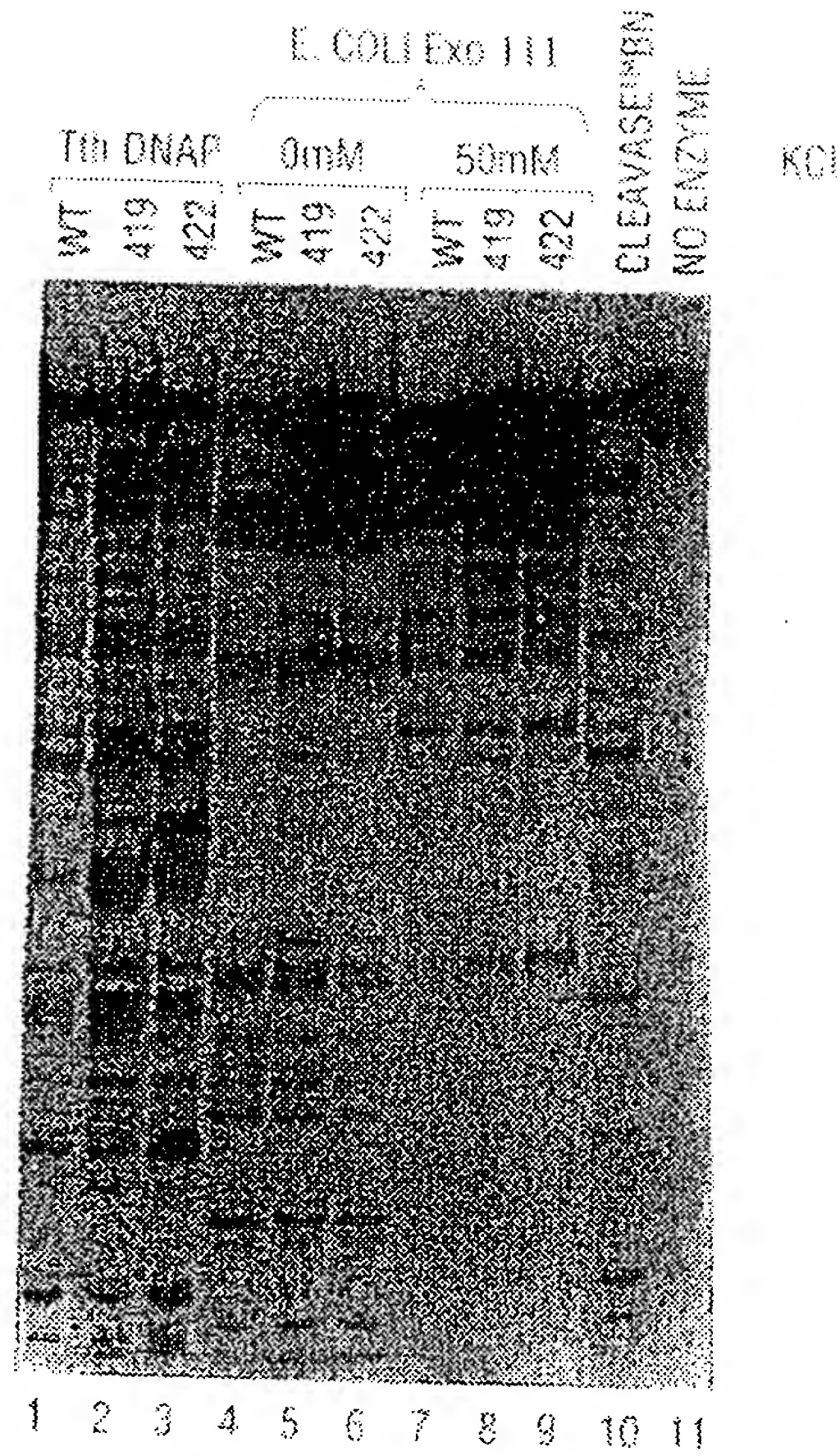
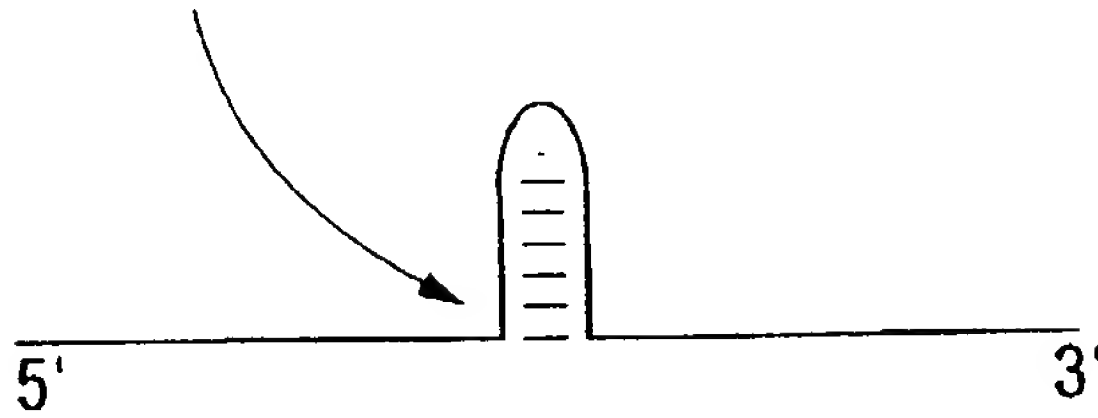
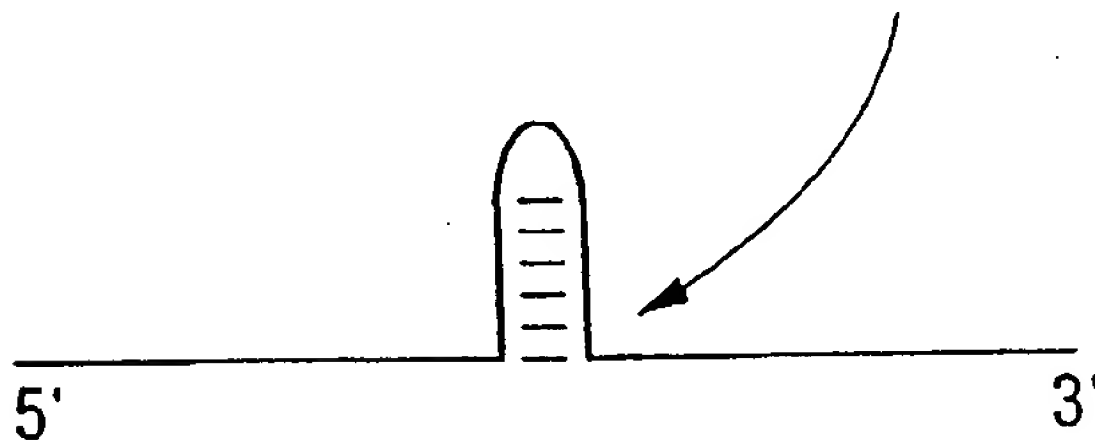


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE



**FIG. 71**

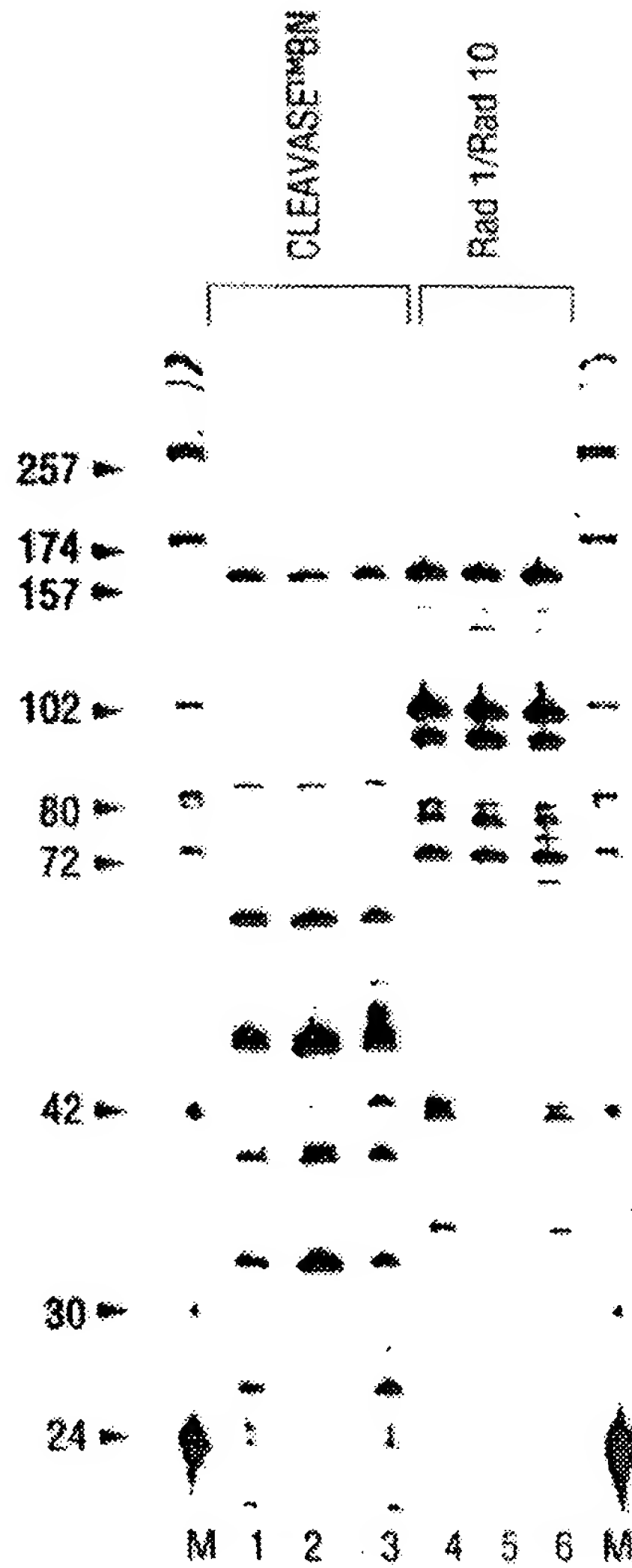


FIG. 72

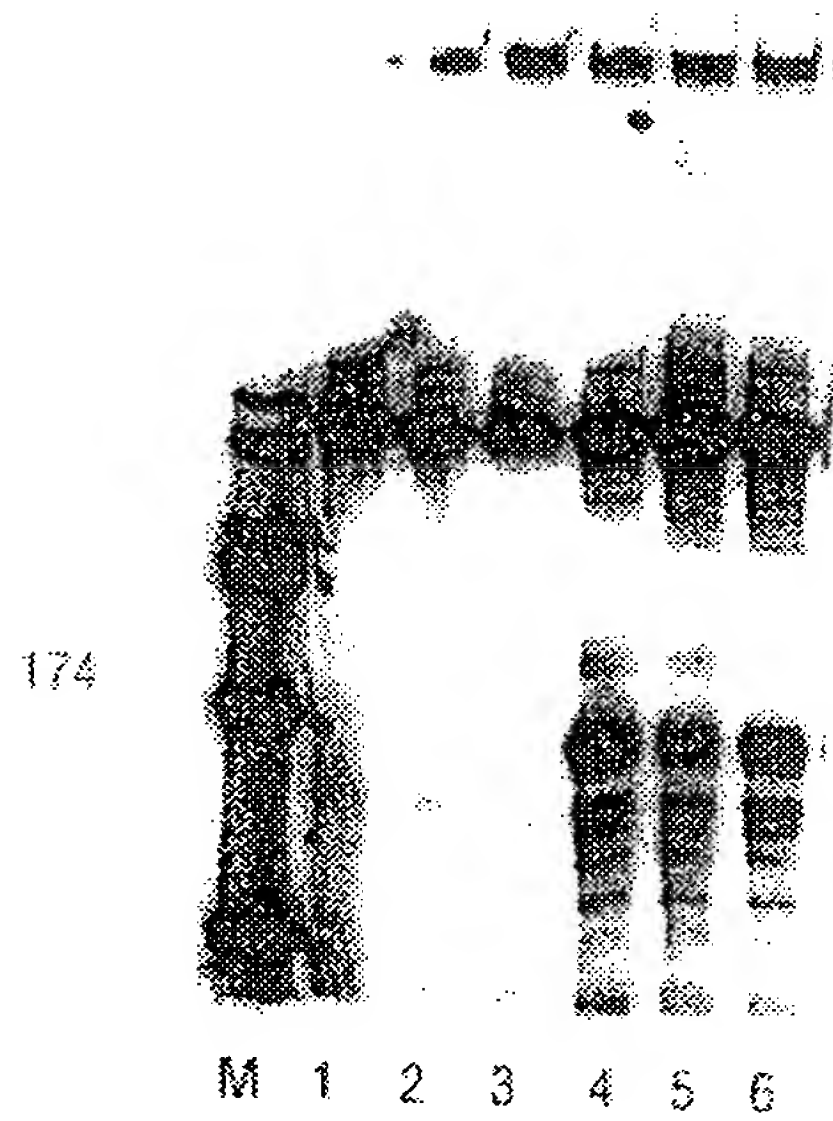


FIG. 73

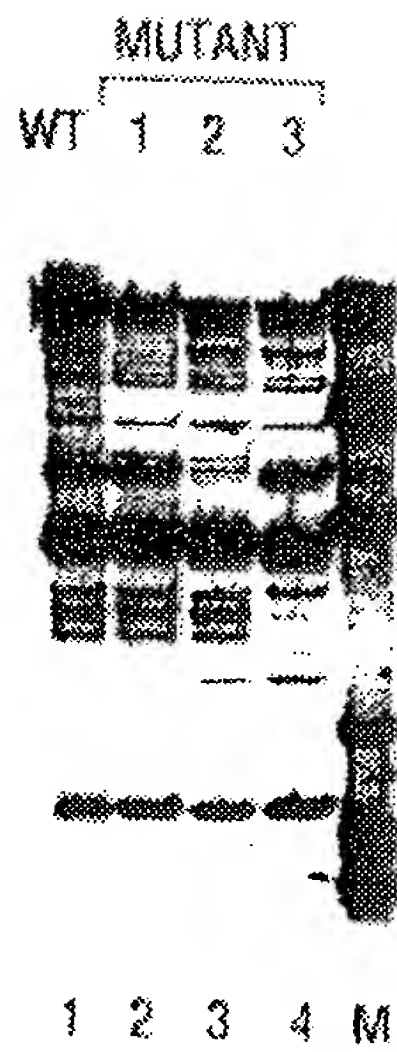


FIG. 74A

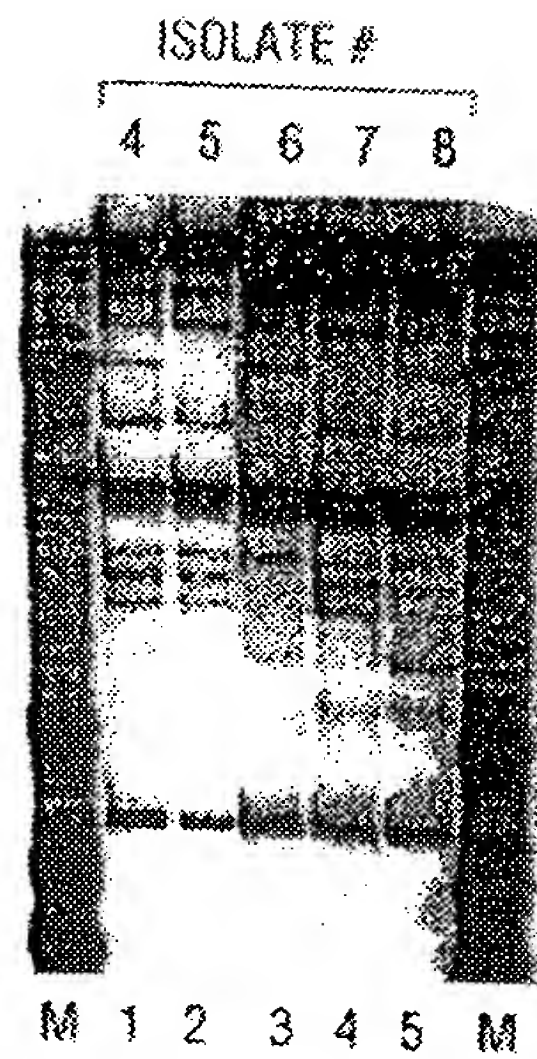


FIG. 74B

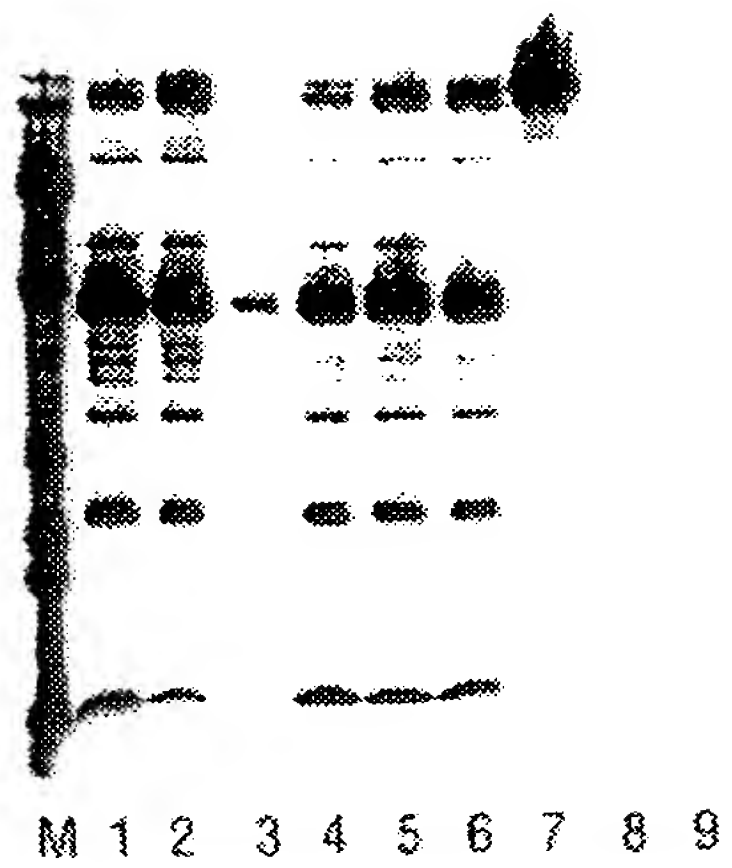


FIG. 75



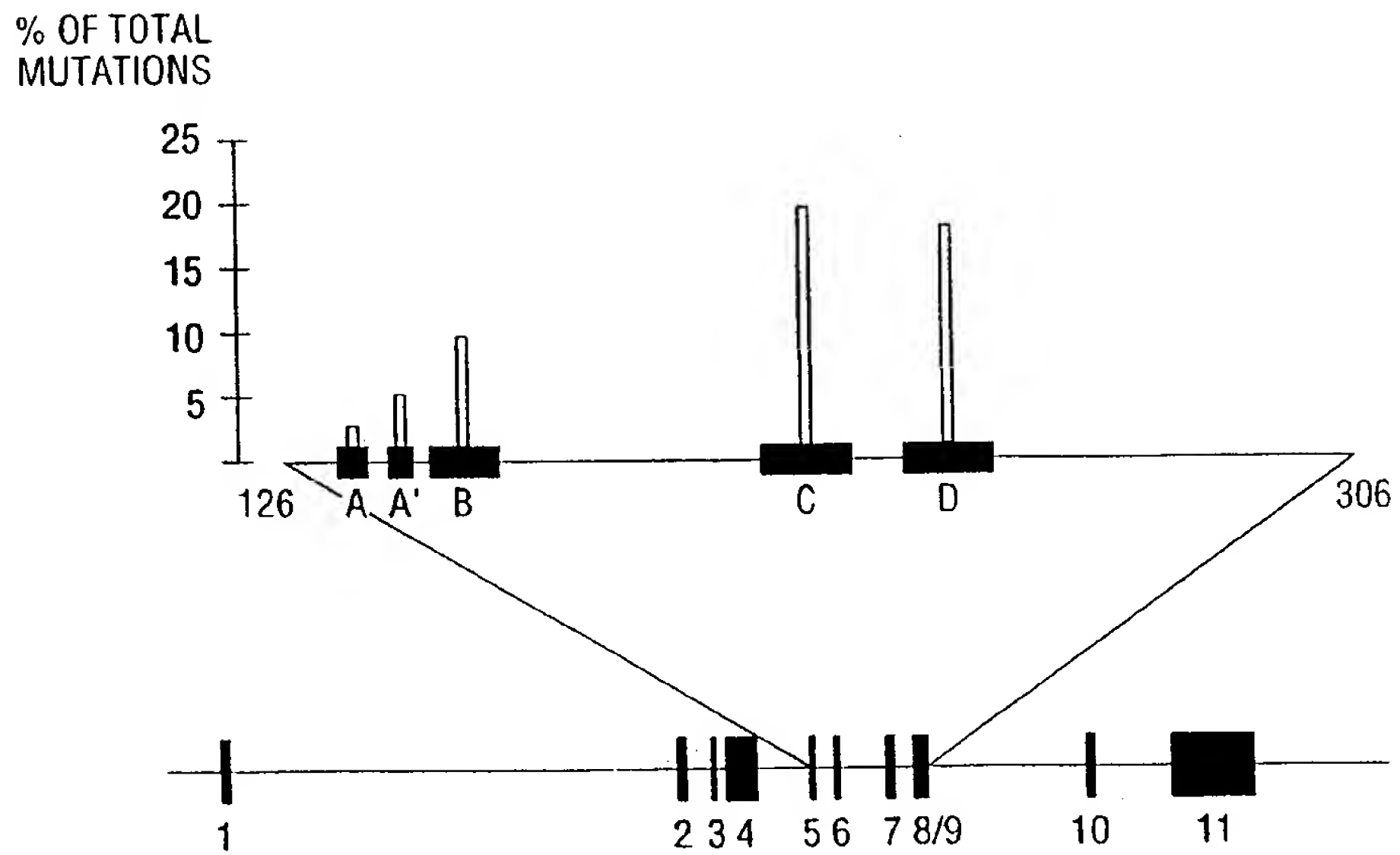


FIG. 76

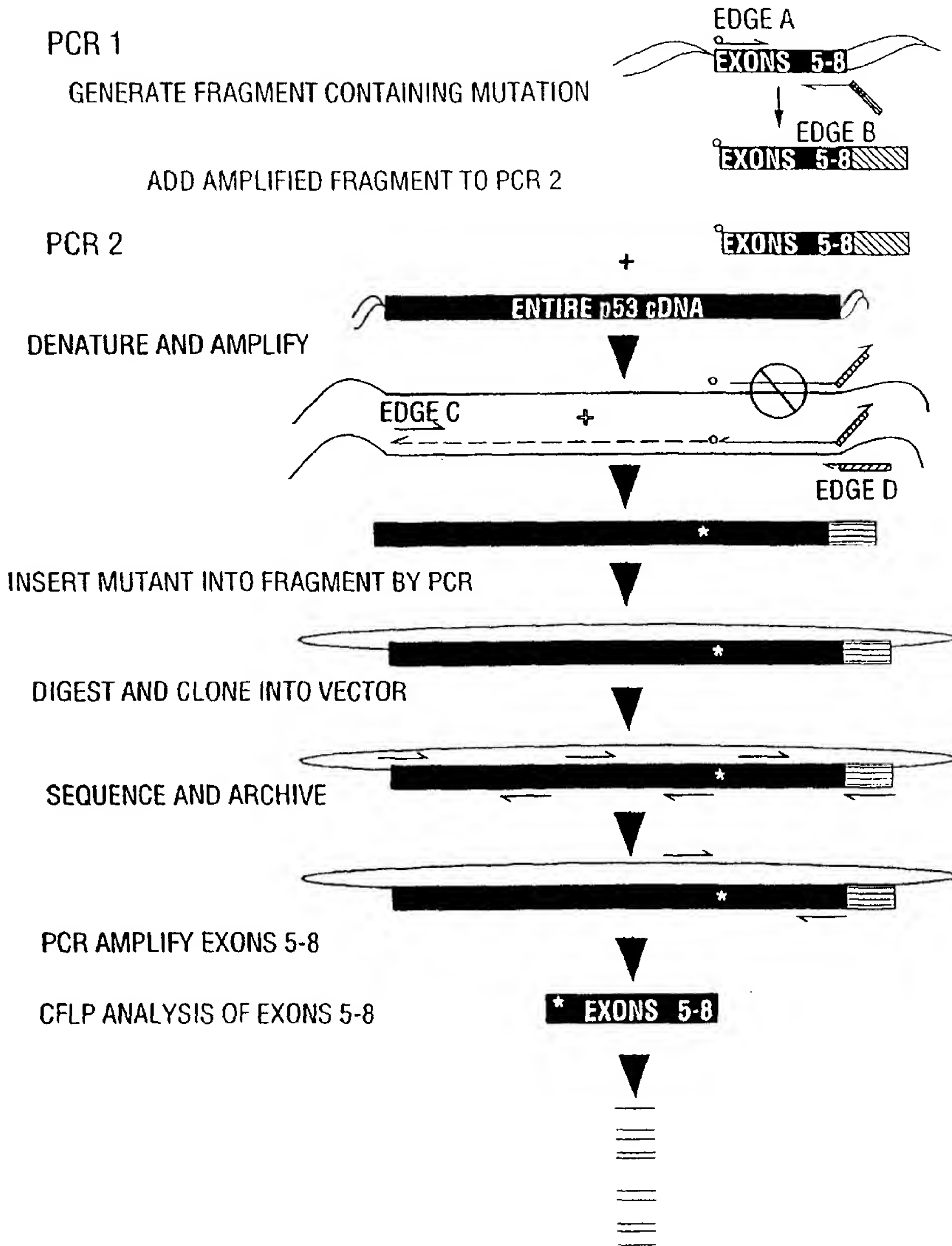


FIG. 77

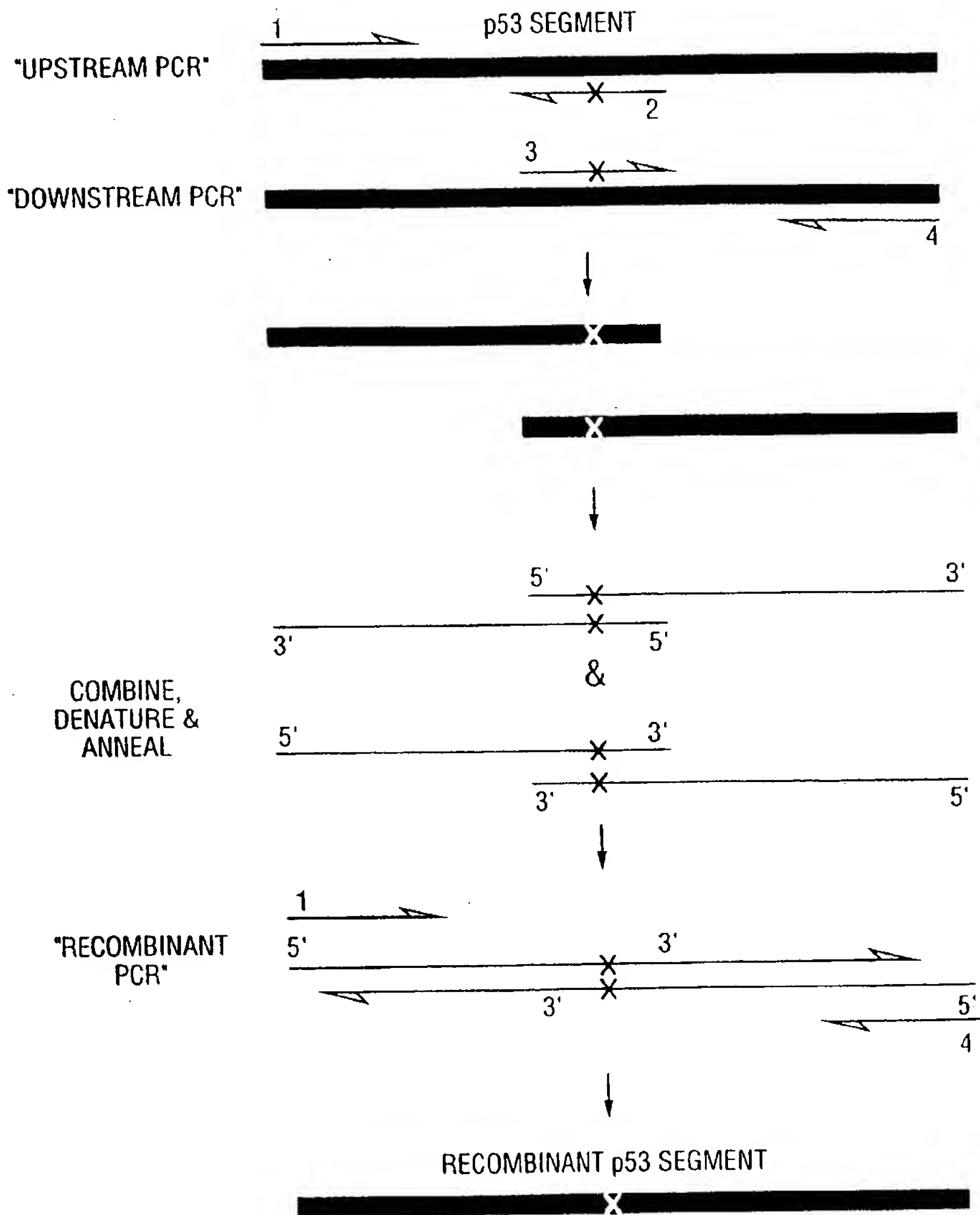


FIG. 78

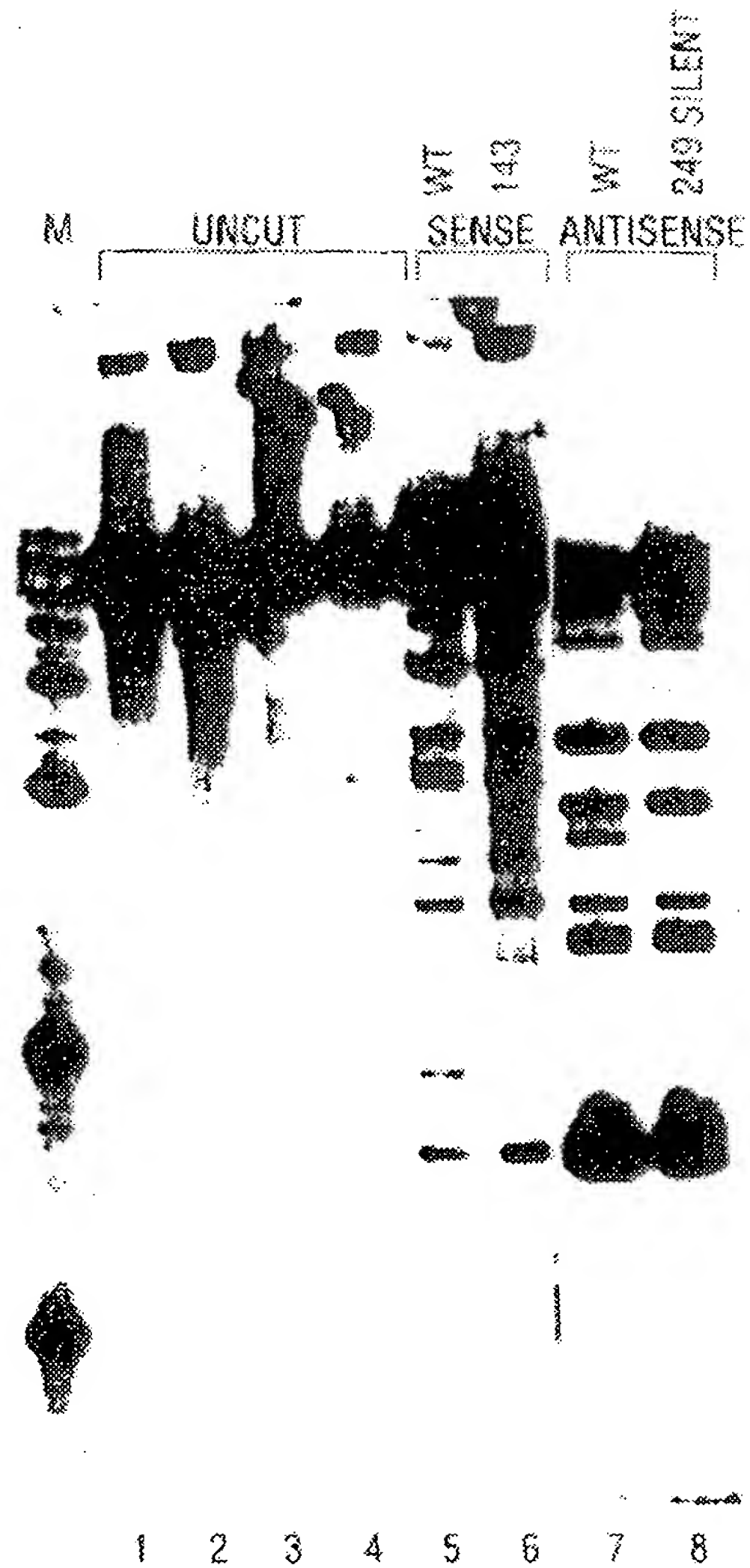


FIG. 79

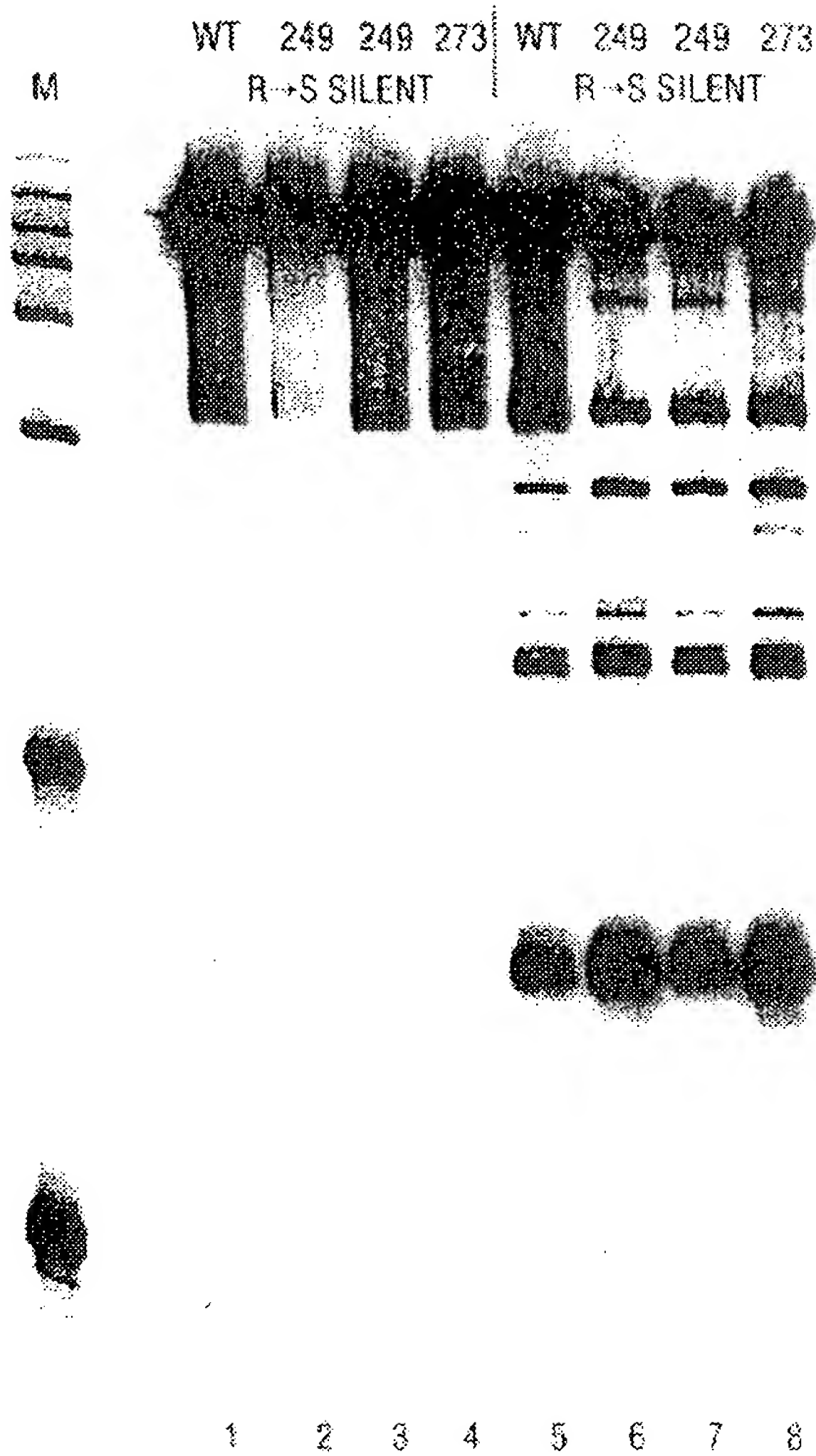


FIG. 80

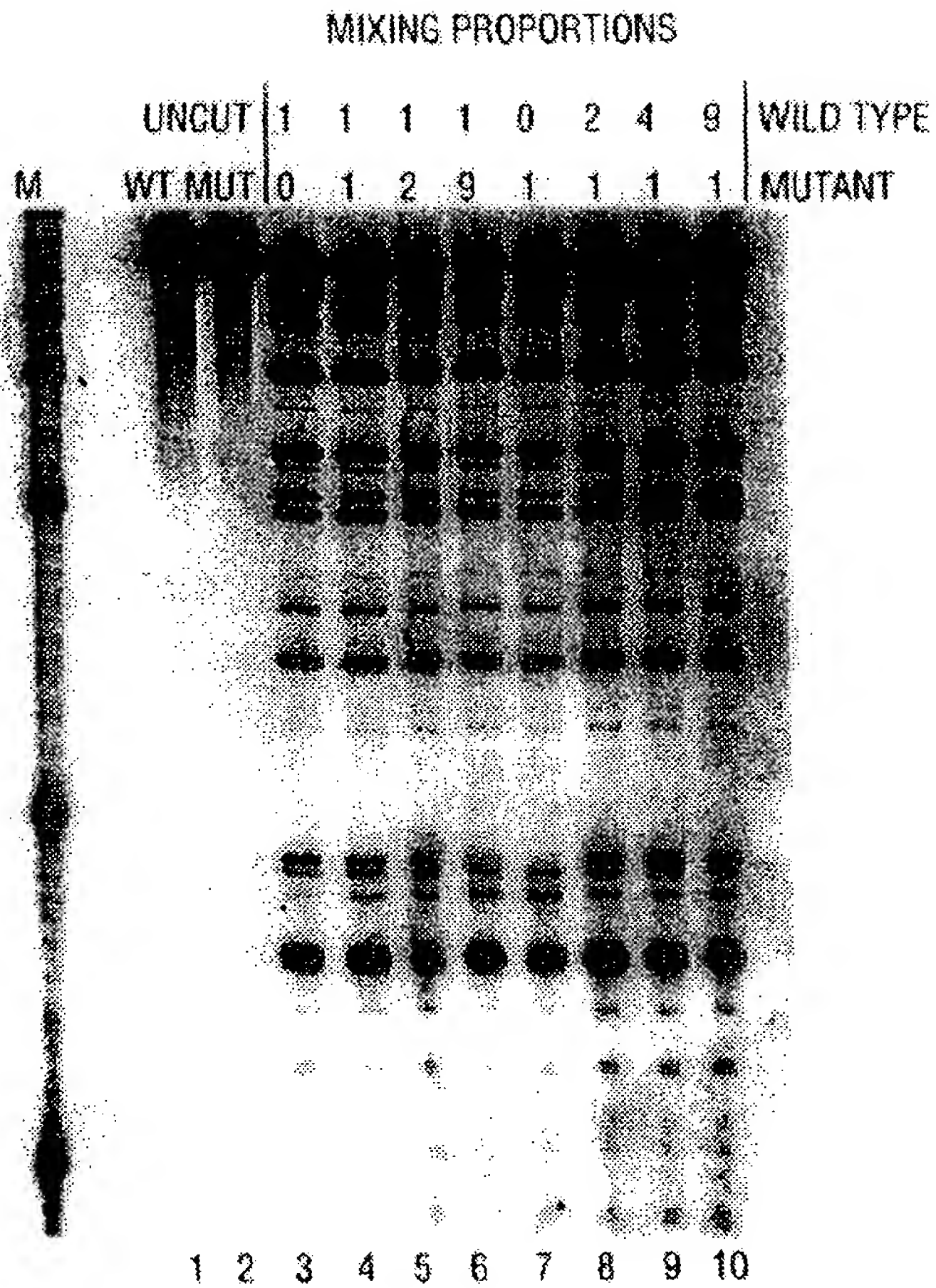


FIG. 81

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGT <u>A</u>	
HCV7.1	(SEQ ID NO:126)		CTGTCTTTCAC	GCAGAAAGCG	<u>CTAGCCATG</u>	GCGTTAGTAT	GAGTGTCTGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	<u>GTGGATGIAA</u>	
HCV6.1			GGTGAGTACA	CCGGAATTGC	<u>CGGGAAGACT</u>	GGTCCCTTTC	TTGGAT- <u>AAA</u>	
HCV7.1			GGTGAGTACA	CCGGAATCGC	<u>IGGGGIGACC</u>	GGTCCCTTTC	TTGGAG-CAA	

FIG. 82A

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B



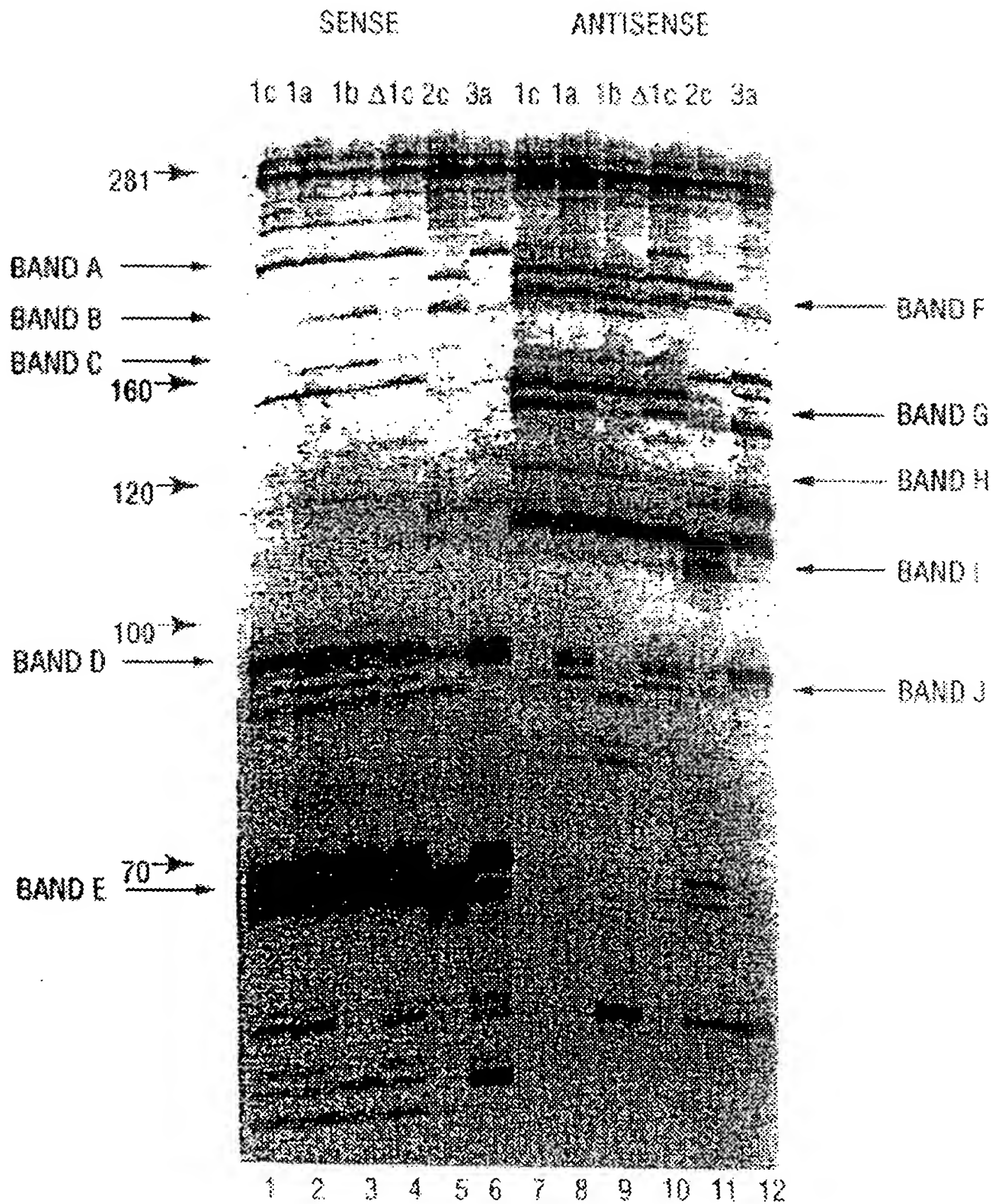


FIG. 83

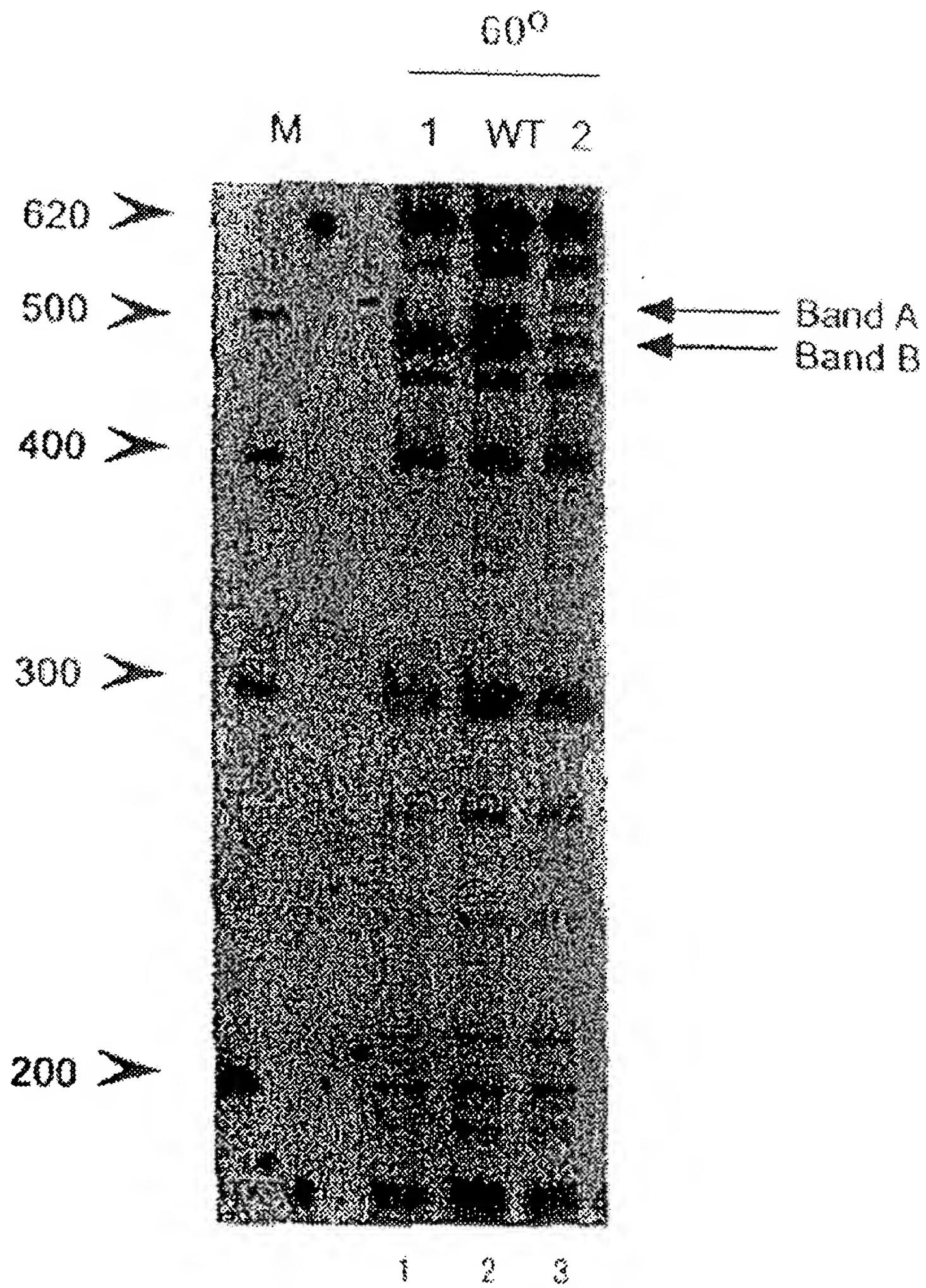


FIG. 84

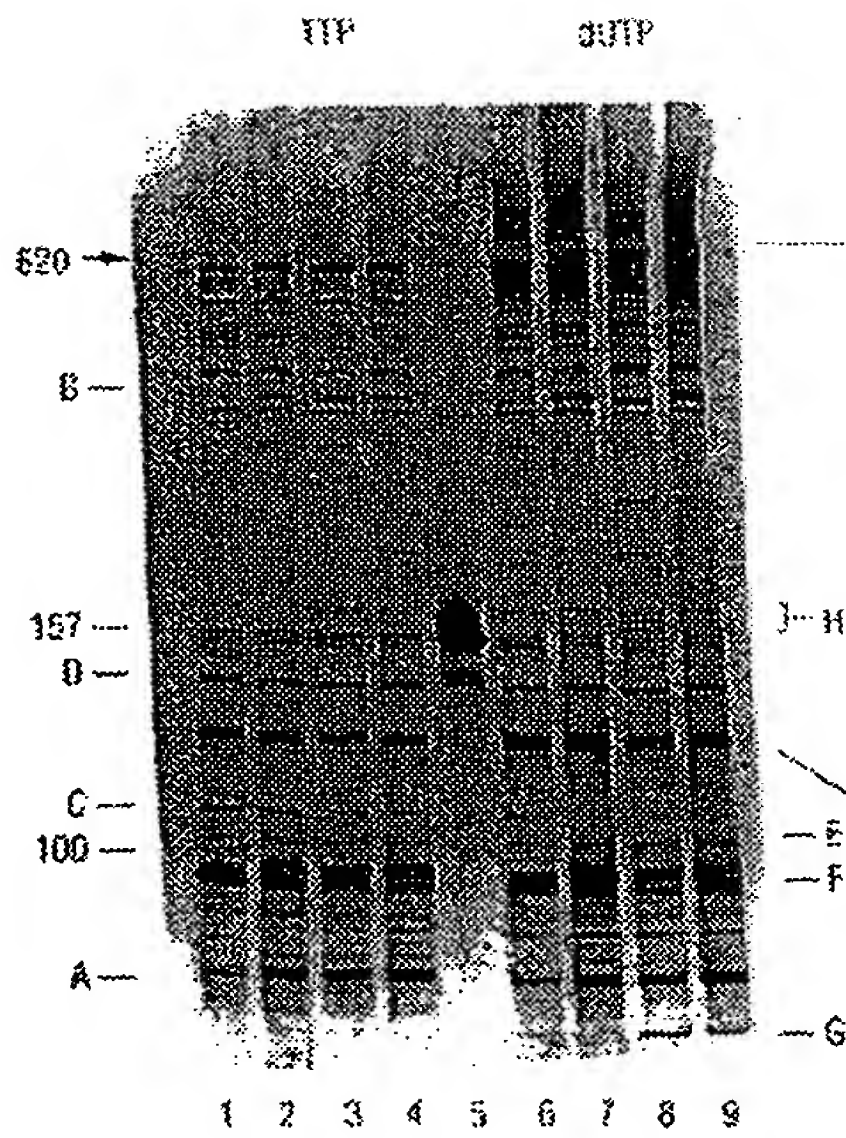


FIG. 85A

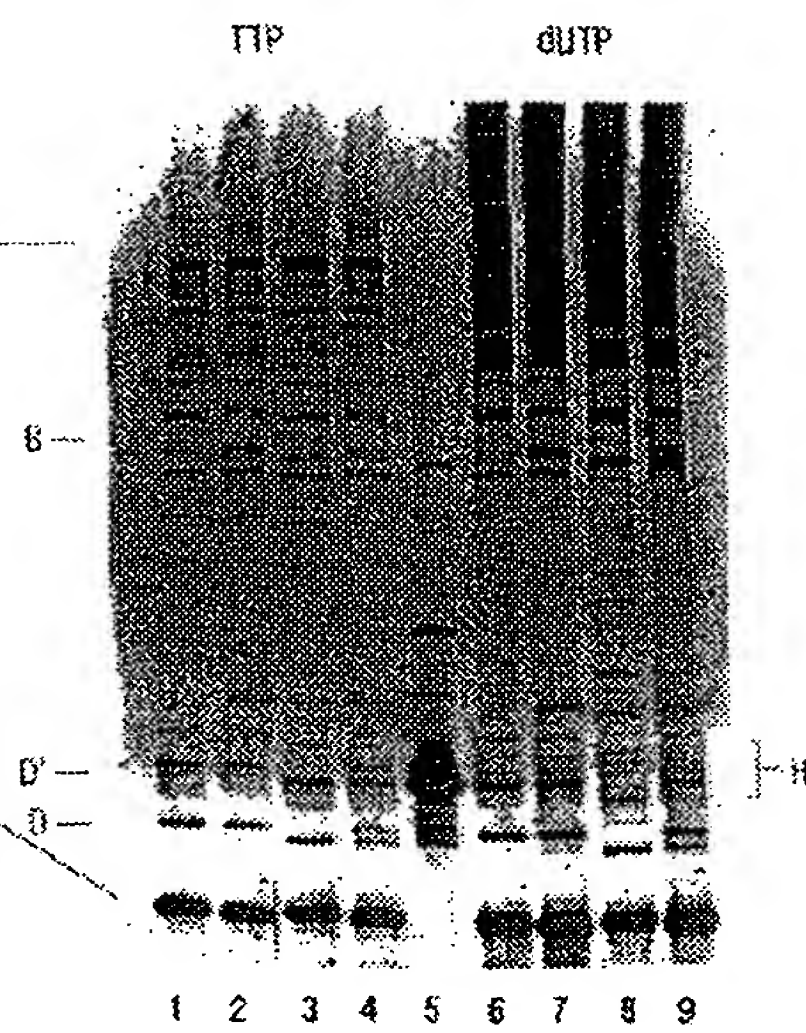


FIG. 85B

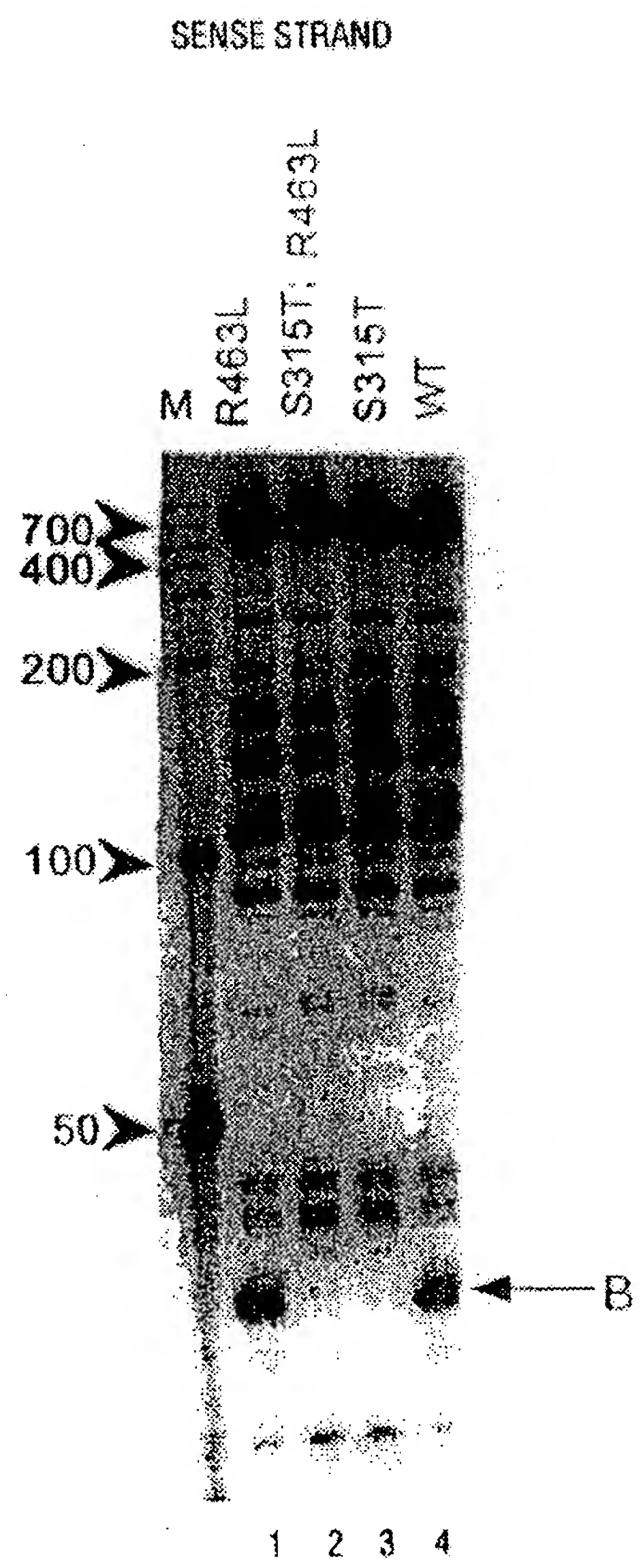


FIG. 86

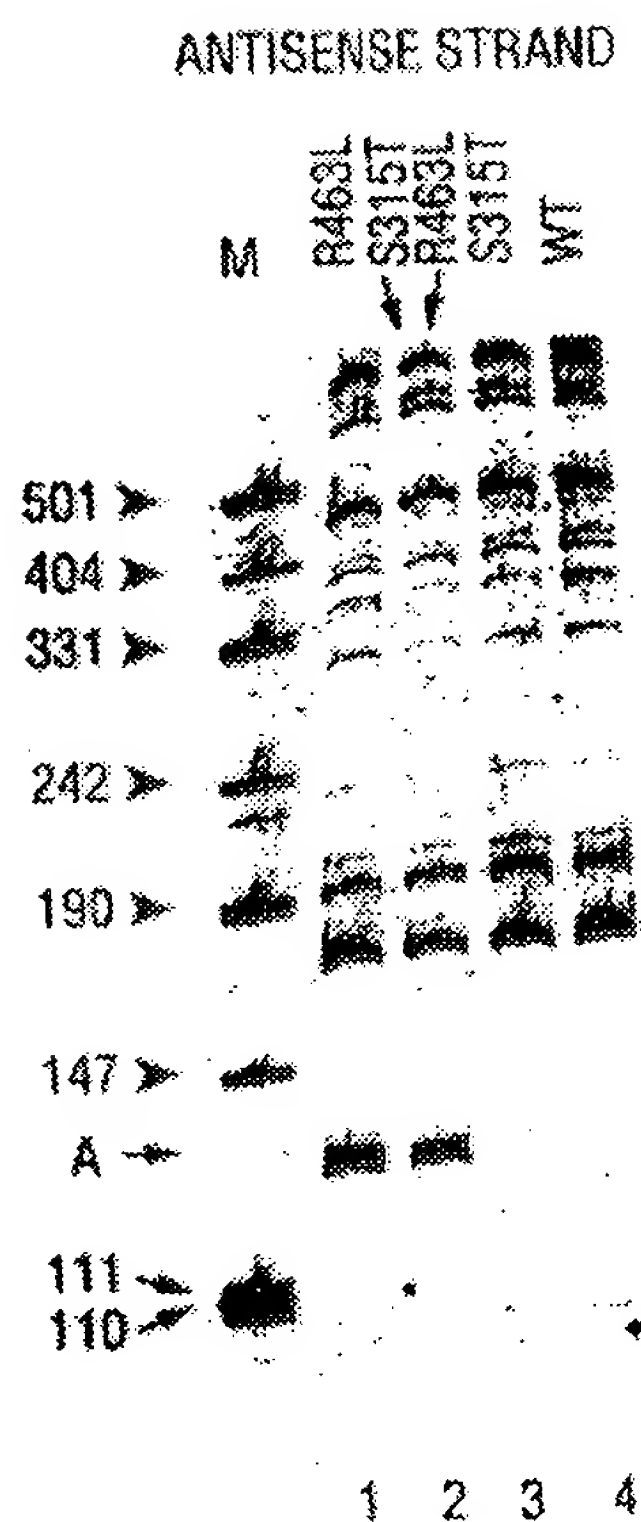


FIG. 87

10	20	30	40	50	60	1638
AGA GTTTGATCCT GGCTCAG						
AAATTGAAGA GTTTGATCAT <u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCTA	ACACATGCAA			
TTTAACTTCT CAAACTAGTA CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT			
70	80	90	100	110	120	ER10
GTCGAACGGT AACAGGAAGA AGCTTGCTTC	TTTGCTGACG	AGTGGGGAC	<u>GGGTGAGTAA</u>			
CAGCTTGCCA TTGTCCCTTCT TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCATT			
130	140	150	160	170	180	
TGTCTGGGAA ACTGCCCTGAT GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT			
ACAGACCCCTT TGACGGACTA CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA			
190	200	210	220	230	240	
AACGTCGCCAA GACCAAAGAG GGGGACCCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCCAGATG			
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC			
250	260	270	280	290	300	
GGATTAGCTA GTAGGTGGGG TAACGGCTCA	CCTAGGCGAC	GATCCCCTAGC	TGGTCTGAGA			
CCTAATCGAT CATCCACCCC ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT			
310	320	330	340	350	360	
GGATGACCAG CCACACTGGA ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG			
CCTACTGGTC GGTGTGACCT TGA	GGATGCCCCTC	CGTGGTCA	CGTGGTCA			
						1659

FIG. 88A



370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCCGACTA	CGTCGGTACG	GGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCGC	ATTTCGCGTG	CGTCCGCCAA	ACAATTCACT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCCTT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACCTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTTCG	CACCCCTCGT

FIG. 88B

790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAAACGAT	GTCGACTTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCATTTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA	CCGAAGGCCT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGACGGGGGC	CCGCACAAGC	GGTGGAGCAT	GTGGTTTAAT
TCCAATTTTG	AGTTTACTTA	ACTGCCCCCG	GGCGTGTTCC	CCACCTCGTA	CACCAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTGCCCT	CGGGAAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTCAGCT	CGTGTGTGTA
TTACACGGAA	GCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
AATGTTGGGT	TAAGTCCCGC	<u>AACGAGCGCA</u>	ACCCTTATCC	TTTGTTGCCA	GCGGTCCGGC
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG
1150	1160	1170	1180	1190	1200
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAACCTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGATG	<u>ACGTCAAGTC</u>
GCCCTTGAGT	TTCCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCA

5B-1

SB-3 SB-4

FIG. 88C

09910925.022602



1210	1220	1230	1240	1250	1260	
ATCATGGCCC TTA						SB-3
ATCATGGCCC TTACGA						SB-4
ATCATGGCCC <u>TTACGACCAG</u>	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG		
<u>TAGTACCGGG</u> AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC		
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC		
TGGAGCGCTC TCGTTCGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG		
1330	1340	1350	1360	1370	1380	
TCGACTCCAT GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT		
AGCTGAGGTA CTTCAGGCCT	AGCGATCATT	AGCACCTAGT	<u>CTTACGGTGC</u>	<u>CACTTATGCA</u>		1743
			GC	CACTTATGCA		
1390	1400	1410	1420	1430	1440	
TCCCGGGCCT TGTAACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT		
<u>AGGGCCCCGA</u> ACAIGTGTGG	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA		
AGGGCCCCGA ACATG						1743
1450	1460	1470	1480	1490	1500	
AGCTTAACCT TCGGGAGGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA		
TCGAATTGGA AGCCCTCCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT		
1510	1520	1530	1540	1550		
CAAGGTAACC GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....			
GTTCCATTGG CATCCCCTTG	GACGCCAACC	TAGTGGAGGA	AT.....			

FIG. 88D

1638 (SEQ ID NO:151)	AGAGTTTGATCCTGGCTCAG
E.colirrsE(SEQ ID NO:158)0	...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCA
Cam.jejun5(SEQ ID NO:159)0	~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCCTAATACATGCA
Stp.aureus(SEQ ID NO:160)0	..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCCTAATACATGCA
ER10 (SEQ ID NO:152)	
E.colirrsE	GGCGGACGGG
Cam.jejun5	60 AGTCGAACGGTAACAG- <u>---</u> GAAGAAGCTTGCTTCTTT- <u>---</u> GCTGACGAGTGGCGGACGGG
Stp.aureus	62 AGTCGAACCGAT- <u>---</u> GAAGCTTCTAGCTTGCTAGAGTGGA- <u>---</u> TTAGTGGCGCACGGG
	61 AGTCGAGCGAA- <u>---</u> CGGACGAGAAGCTTGCTTCTCTGATG- <u>---</u> TT-AGCGGCGGACGGG
ER10	TGAGTAA
E.colirrsE	114 TGAGTAAATGCTCTGGGA-AACTGCCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATA
Cam.jejun5	114 TGAGTAAAGGTATAGTTAATCTGCCCTACACAAAGAGGACAACAGTTGGAAACGACTGCTAATA
Stp.aureus	113 TGAGTAACACGCTGGATAACCTACCTATATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA
E.colirrsE	175 CCGCATAAC- <u>---</u> GTGCAAGAC- <u>---</u> CAAAGAGGGGACCTTCG- <u>---</u> GGCCTCTTG
Cam.jejun5	176 CTCTATACTCCTGCTTAAACACAAGTTGAGTAGG- <u>GAAAG-<u>---</u>TTT</u> TT- <u>---</u> CG
Stp.aureus	175 CCGGATAATATTTTGAAACCGCATGGTTCAAAAGTGAAAGACGGT- <u>---</u> CTT- <u>---</u> GCTGTCA
E.colirrsE	221 CCATCGGATGTGCCCAGATGGGATTAGTAGTGGGTAAACGGCTCACCTAGGCGACGA
Cam.jejun5	221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACC AAGGCTATGA
Stp.aureus	229 CTTATAGATGGATCCGGCTGCCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACC AAGGCAACGA
E.colirrsE	283 TCCCTAGCTGGTCTGAGAGGATGACCCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
Cam.jejun5	283 CGCTTAAC TGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTA
Stp.aureus	291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
1659 (COMPL)	ACTCCTA

FIG. 89A

E.colirrsE	345	CGGAGGCAGCAGTGGGGAATATTGCACAAATGGGCGCAAGCCTGATGCAGCCATGCCCGCGTG
Cam.jejun5	345	CGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCCCTGACGCAACACGCCCGCGTG
Stp.aureus	353	CGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCCGCGTG
1659(COMPL)		CGGAGGCAGCAG
E.colirrsE	407	TATGAAGAAGGCCTTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
Cam.jejun5	407	GAGGATGACACTTTTTCGGAGCGTAAACTCCTTTTCTTAGGGAAG <u>-----AATT</u>
Stp.aureus	415	AGTGATGAAGGTCTTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACATATGTGTAGTAAC
E.colirrsE	468	ACCTTTGCTCATTGACGTTACCCGCGAGAAGACCGGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5	455	C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Stp.aureus	476	<u>-TGTCACATCTTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG</u>

FIG. 89B

E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGGGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTTGTGAATCTAATGGCTTAACCATTTAAACTGCTTGGGAACCTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAGCCACGGCTCAACCGTGGAGGTCATTGGAAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGTAGAATTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAGTGGAAATTCATGTGTAGCGGTGAAATGCCGACAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGGGGCCCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCCGAAGGCGATCTGCTGGAACCTCAACTGACGCTAAGGCCGGAAGCGTGGGGA
Stp.aureus	724	ACACCAGTGGCGAAGGCGACTTTCTGCTGTAACTGACGCTGATGTGCCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTAGGGG

FIG. 89C

E.colirrsE	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
Cam.jejun5	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAGTGTAACCGCCTGGGGAGTACGGTCGC
Stp.aureus	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCCTGGGGAGTACGACCGC
E.colirrsE	900	AAGGTTAAACTCAAATGAATTGACGGGGGCCGCACAAGCGGTGGAGCATGTGGTTTAATT
Cam.jejun5	876	AAGATTAAACTCAAAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATT
Stp.aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATT
E.colirrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAAT
Cam.jejun5	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAAACCTTTTAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGCGAAGAACCTTACCAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
E.colirrsE	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAAGTCTCGTTGTGA
Cam.jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTCAAGTCTCGTTGTGA
Stp.aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCATGGTTGTCGTCAAGTCTCGTTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrsE	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTTAGTTGCTAACGGTTCCGG-CC
Stp.aureus	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

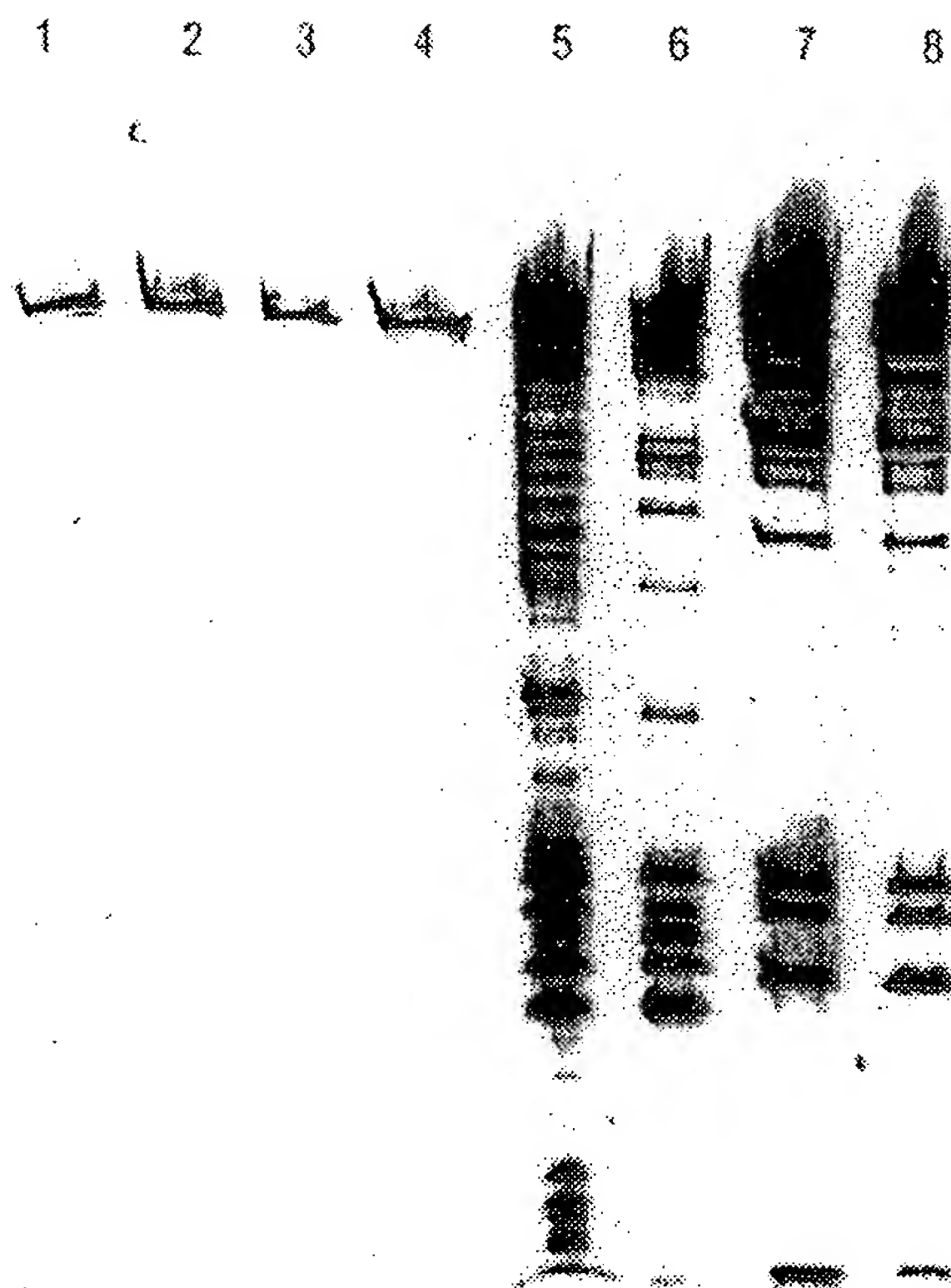
FIG. 89D

SB-3 (SEQ ID NO:157)		ATGACGTCAAGTCATC
SB-4 (SEQ ID NO:154)		ATGACGTCAAGTCATC
E.colirrsE	1142	GGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGATGACGTC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTC
Stp.aureus	1152	GGGCACTCTAAGTTGACTGCCCGTGACAAACCGGAGGAGGTGGGATGACGTC
SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTACGA
E.colirrsE	1204	ATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGGACCTC
Cam.jejun5	1183	ATGGCCCTTATGCCAGGGCGACACACGTGCTACAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGGCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAACC
E.colirrsE	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GCGAGGTGGAG-CAAACTCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGAGGTCAAGCAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743(compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E

E.colirrsE	1389	CTTG	TACACACCGCCCGTCACACCATGGGAGTGGGTGCAAAAGAGTAGGCTTAACCT
Cam.jejun5	1368	CTTG	TACTCACC GCCCGTCACACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT- <u>A</u> -A
Stp.aureus	1399	ATTG	TACACACCGCCCGTCACACACCGAGAGTTTGTAACACCCGAGCCGGTGGAGTAACCT
1743 (compl)		CTTG	TAC
E.colirrsE	1451	TCG- <u>GG</u>	AGGCGCTTACCACCTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam.jejun5	1427	AC- <u>---</u>	T-AGTTACCGTCCACAGTGGAAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp.aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAAGCCG	
E.colirrsE	1512	TAGGGGAACCTGCGGGTTGGATCACCCTCCTTA---	
Cam.jejun5	1485	TAGGAGAACCTGCGGGTTGGATCACCCTCCT-----	
Stp.aureus	1523	TATCGGAAGGTGCGGCTGGATCACCCTCCTTTCT-	

FIG. 89F

**FIG. 90**



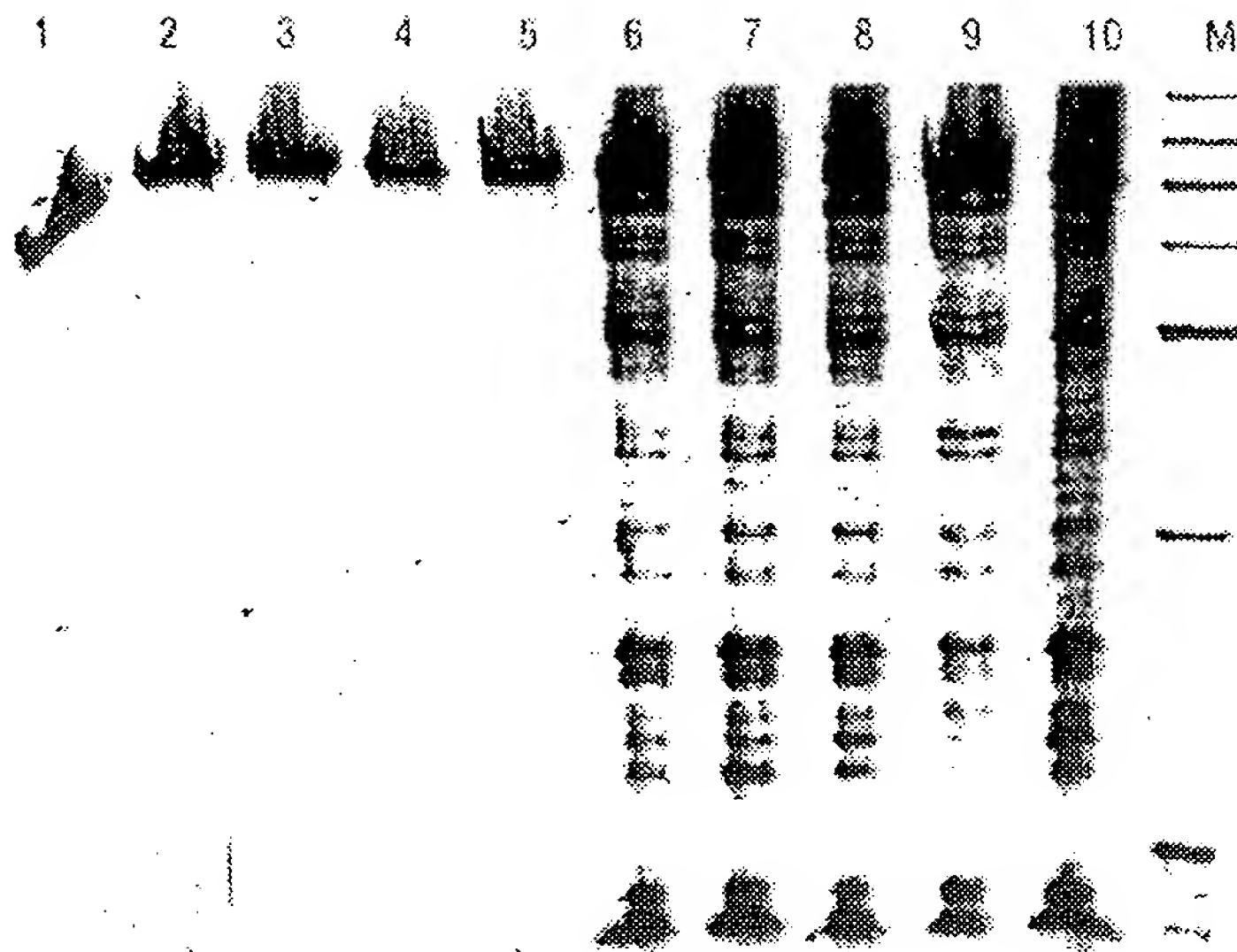


FIG. 91A

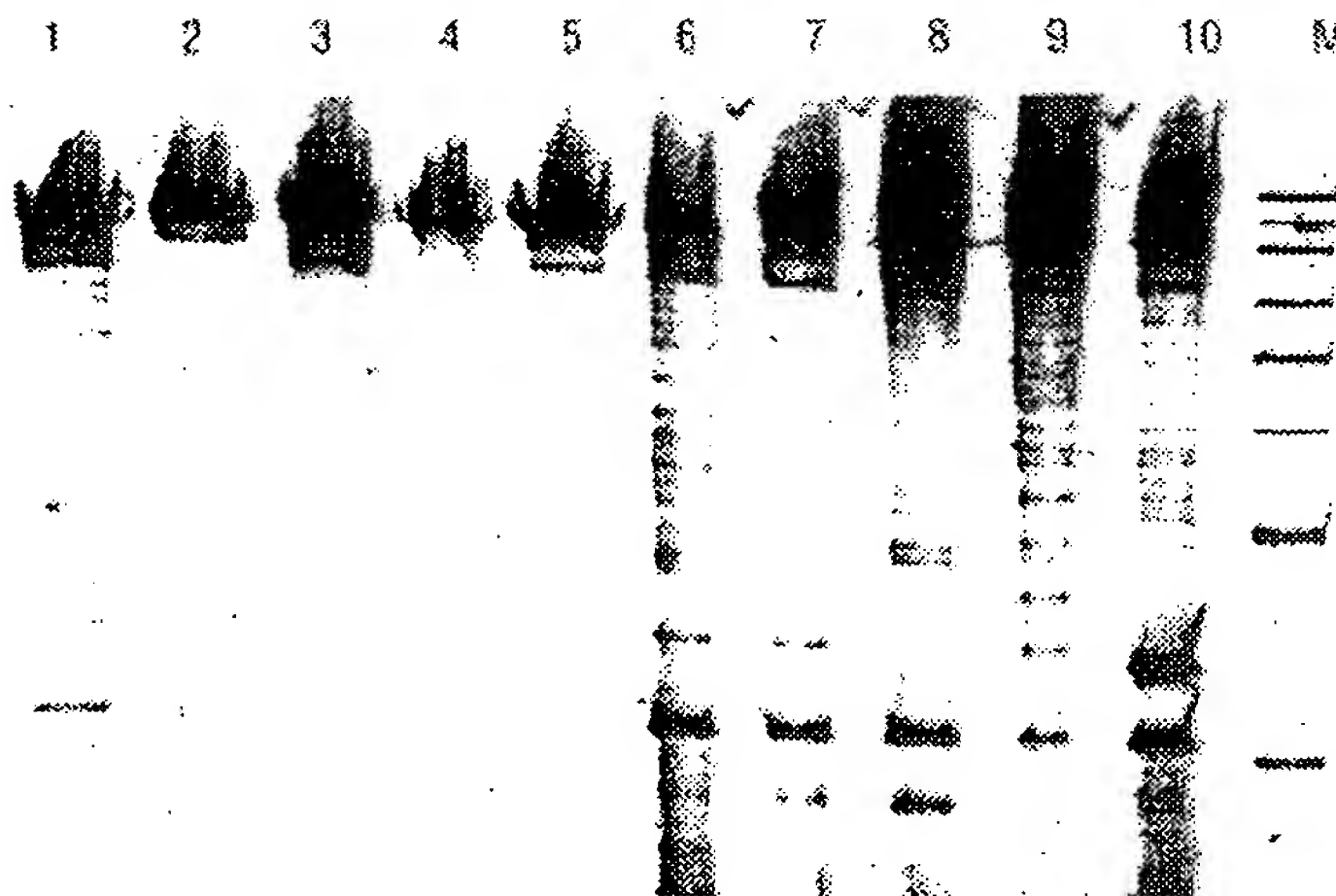


FIG. 91B

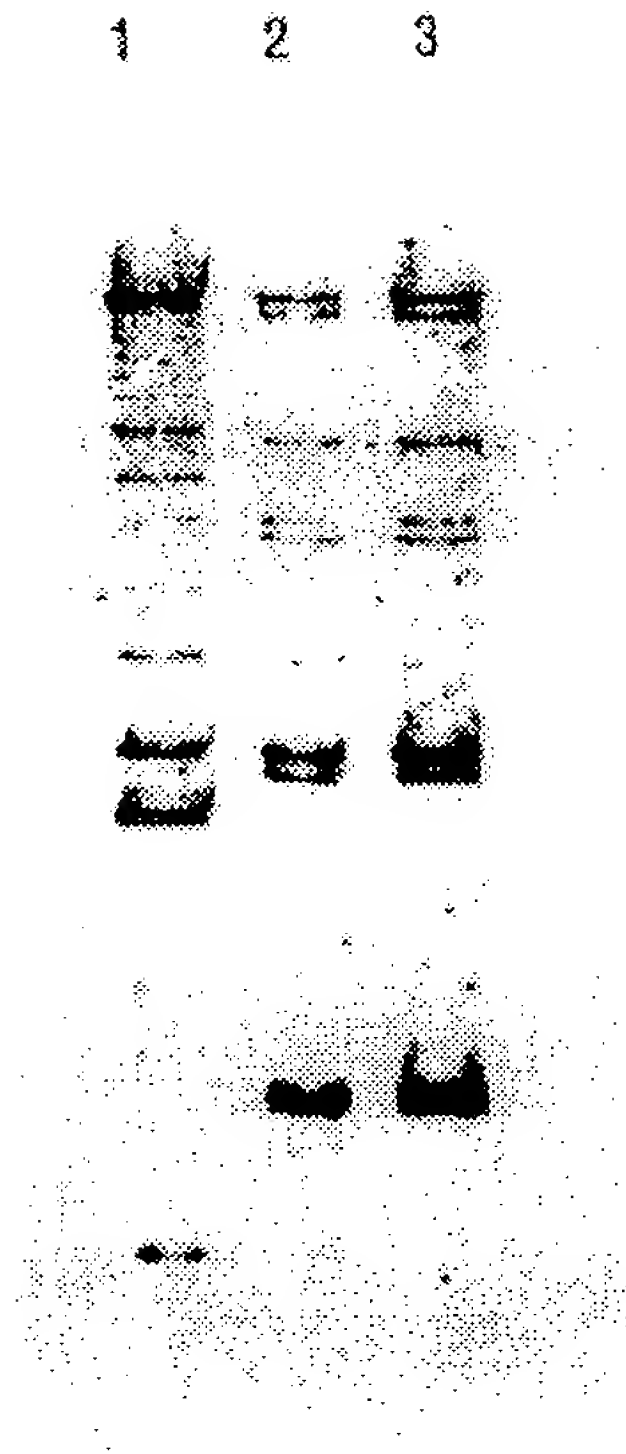


FIG. 92

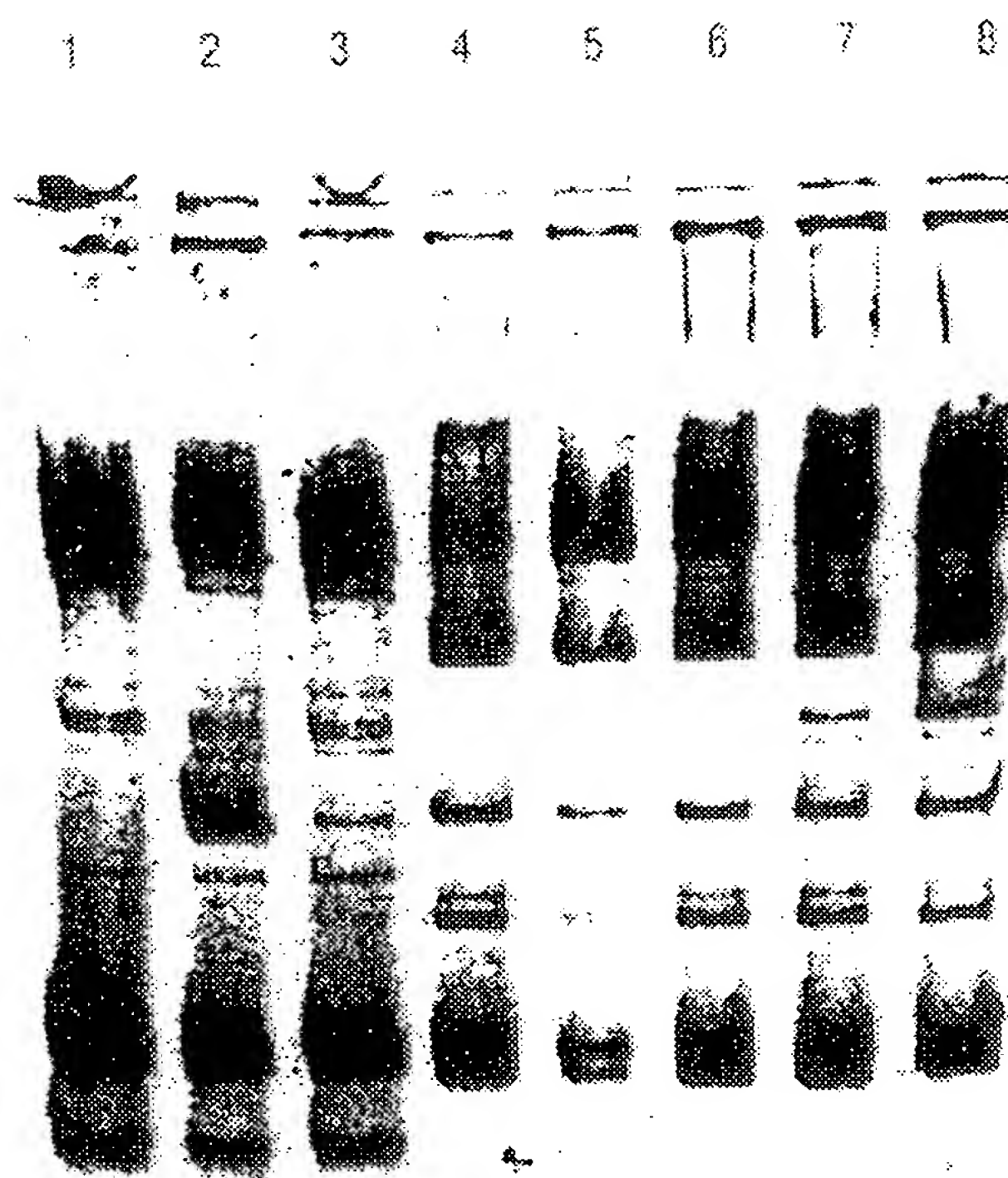


FIG. 93

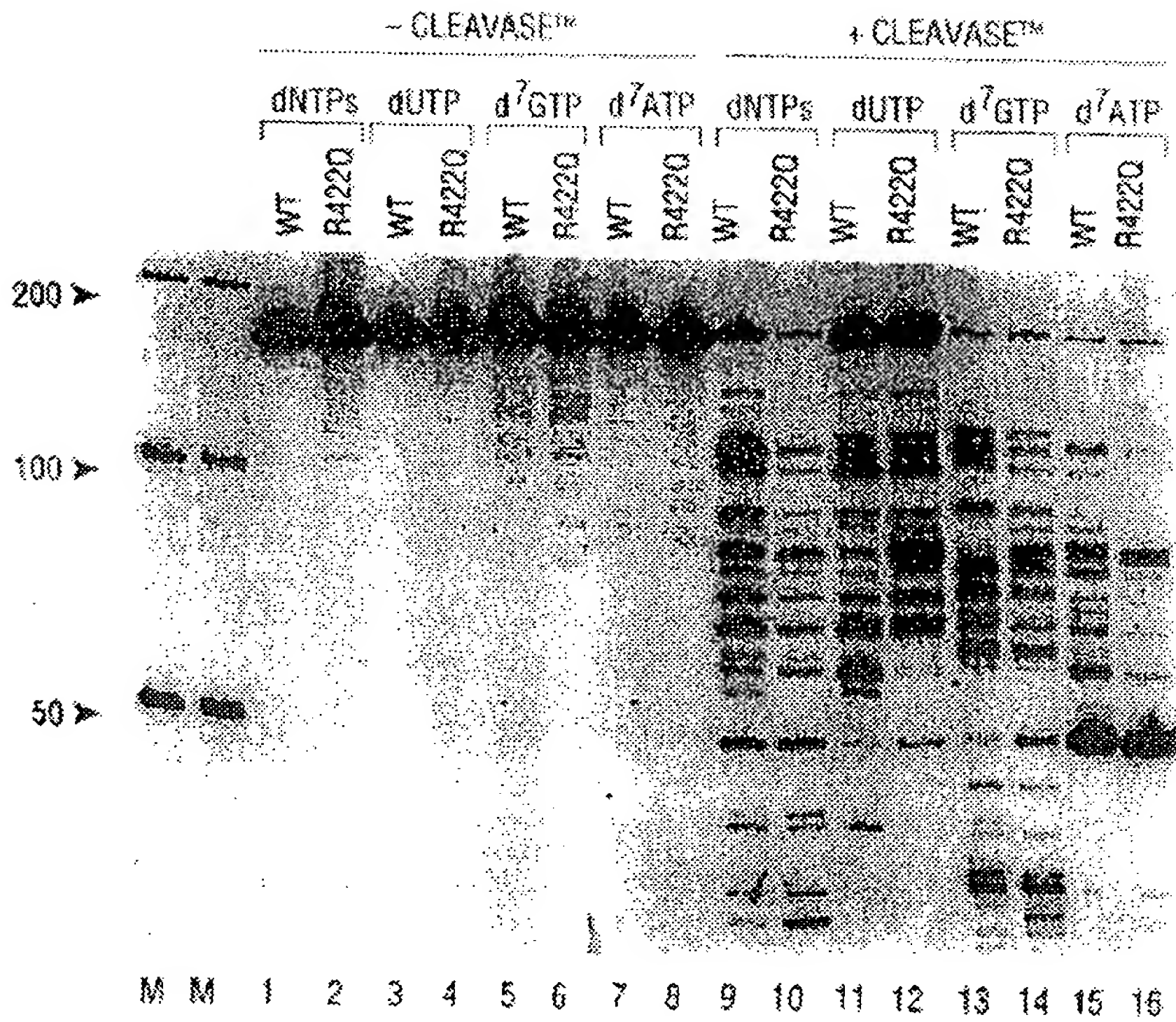


FIG. 94